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GenCore version 5.1.7
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                  Copyright
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OM protein - protein search, using sw model

April е 6 Run

6, 2006, 10:12:19; Search time 260.97 Seconds (without alignments) 361.981 Million cell updates/sec

US-10-717-984-1 1149

Perfect score:

1 MGKGDPKKPRGKMSSYAFFV......DEBEEDBEDBDBEEDDDDB Scoring table: Sequence:

215

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

2443163

length: 0 length: 2000000000 DB seq Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* Geneseg 21:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ole (SUMMARIES		
Result No.	Score	Match	Query Match Length	B B	ID	Description	uc
н	1149	100.0	215	ဖ	ABU07499	Abu07499 P	Protein d
7	1149	100.0	215	9	AAE35859	Aae35859 H	Human HMG
m	1149	100.0	215	7	ADD40789	Add40789 H	Human HMG
4	1149	100.0	215	7	ADD40788	Add40788 H	Human HMG
S	1149	100.0	215	7	ABM85677	Abm85677 H	Human pro
9	1149	100.0	215	80	ADO60491	_	Human hig
7	1149	100.0	215	80	AD025918	_	Human hig
8	1149	100.0	215	œ	AD071477	Ado71477 H	Human hig
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10	1149	100.0	215	8	ABM81508	_	Tumour-as
11	1149	100.0	215	0	ADW81011		Amphoteri
12	1149	100.0	215	σ	ADX69343		Human amp
13	1149	100.0	215	σ	ADY14248	Ady14248 P	PRO polyp
14	1149	100.0	215	σ	ADY85326		Human hig
. 15	1149	100.0	215	σ	ADY85085		Human HMG
16	1149	100.0	215	σ	ADZ80804		Amino aci
17	1144	9.66	214	7	ADD47645	Add47645 H	Human Pro
18	1144	9.66	214	7	ADE60447	Ade60447 H	Human Pro
19	1144	9.66	214	7	ADE57980	_	Human Pro
20	1144	9.66	214	7	ADE57984	Ade57984 H	Human Pro
21	1144	9.66	214	7	ADE60732	Ade60732 H	Human Pro
22	1144	9.66	214	7	ADE60728		
23	1144	9.66	214	80	ADS17580	Ads17580 A	Amino aci

215 5 ABB57220 215 6 AAB35860 215 8 AD025919 215 8 AD071478 215 8 AD071478 215 9 ADW85327 220 7 ABM85676 215 9 ADW85016 215 9 ADW85016 216 9 ADW85016 217 7 ADR5078 214 7 ADR5078 214 7 ADR5078 214 7 ADR5078 214 7 ADR5078 214 7 ADR5078 215 8 AD080179 215 8 AD080179 216 8 AD025935	22.	Add4/643 Kac Froce Ado25919 Mouse/rat Ado71478 Mouse/rat			Ady85029 Rat and m Ady85088 Human HMG	Abp64829 Human pro Ade60730 Rat Prote	Ade57978 Rat Prote Ade57982 Rat Prote		Ado80179 High mobi	
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ALIGNMENTS

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring. Protein differentially regulated in prostate cancer #102. ABU07499 standard; protein; 215 AA. (ORIG-) ORIGENE TECHNOLOGIES INC. 06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P. 08-APR-2002; 2002WO-US010824. (first entry) WPI; 2003-058520/05. N-PSDB; ABX10404. WO200281638-A2. Jay G; 28-JAN-2003 Homo sapiens 17-OCT-2002. ABU07499; Sun Z, RESULT 1

Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 413-414; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.

Ady85051 Human HMG

9 ADY85051

221

9.66

1144

binding motif (HMG1 B box)"

binding motif (HMG1 A box)"

/note= "DNA

Binding-site

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CC (1) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated cativity of a polypeptide differentially regulated in prostate cancer cells with a test agent under conditions effective for the rest agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, assessing, monitoring, prognosticating, preventing or treating, datermining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus cc for searching specific binding partners of the polypeptide and thus cc for searching specific binding partners of the polypeptide. (I) is useful contined and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of targets in these control and disease pathways and the delineation of a protein differentially
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Matches 215; Conservative
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New isolated polypeptide having a vertebrate HWG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetea
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-naturally occurring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatorid arthritis, appendictis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, bronchitis, embhysema, HVV infection, candidiasis, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, enhits, dermatitis, and printiple sclerosis, gout, cerebral infarction, neutitis, Goodpasture's syndrome, graft-versus-host therapy. The present sequence is human HMGI (also termed as HMGBI)
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; Pred. No. 2.7e-93;
0; Mismatches 0;
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              89. .162
/note= "DNA
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Matches 215; Conservative
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120

Location/Qualifiers

Key Binding-site

Homo sapiens

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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or preparation of compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention are used in kit for characterising the status of the endometrium, especially for presence of pregnancy or irregularities in the menstrual cycle. The proteins used in the invention can be HMGB! 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB! 1s RAGE (receptor for advanced glycation end products). The products of the invention have nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products) which is involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometrions or diagnoses of endometrial disease, particularly endometrions or polyps, hyperplasia or carcinoma of the endometrium, particularly for detecting pregnancy or mensitual disorders. This sequence represents the human HMGBl protein used in the method of
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                                                          endometrial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Developing treatment and diagnosis of endometrial disorders, using high mobility group B proteins, or related nucleic acid or interaction partners, as targets.
                                                     high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease, contraceptive; endometrium; pregnancy; menstrual cycle irregularity; RAGE; receptor for advanced glycation end; gynaecological; cytostatic; nuclear transcription factor complex; tumour metastasis; endometriosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 43pp; German.
                                                                                                                                            polyps; hyperplasia; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                19-DEC-2001; 2001DE-01062556.
                                                                                                                                                                                                                                                                                                                      19-DEC-2002; 2002WO-EP014579.
                                                                                                                                                                                                                                                                                                                                                                                                         (ALCE-) ALCEDO BIOTECH GMBH
                 Human HMGB1 protein #2.
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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or group B proteins (EMGB) as target molecules for development or preparation of compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention are used in kit for characterising the status of the endometrium, corrected to presence of pregnancy or irregularities in the menstrual cycle. The proteins used in the invention can be HMGB1, 2 or 3, or ST100-KMG, and the preferred interaction partner for HMGB1, 2 or 3, or ST100-KMG, and the preferred interaction partner for HMGB1; saddE (receptor CC for advanced glycation end products). The products of the invention have gynaecological, contraceptive and cytostatic activity. HMGB is part of nuclear transcription factor complex and, extracellularly, a ligand for the surface RMGE (receptor for advanced glycation end products of the invention are used to cardinally endometrials or polyps, hyperplasia or carcinoma of the endometrium, also contraceptives and methods for assessing status of the endometrium, particularly for detecting pregnancy or menstrual disorders. This sequence represents the human HMGB1 protein used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                              high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease; contraceptive; endometrium; pregnancy; menstrual cycle irregularity; RAGE; receptor for advanced glycation end; gynaecological; cytostatic; nuclear transcription factor complex; tumour metastasis; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developing treatment and diagnosis of endometrial disorders, using high mobility group B proteins, or related nucleic acid or interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDMAKADKARYEREMKTYIPPKGETKKKKKDDNAPKRPPSAFFLFCSEYRPKIKGEHPGL
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100.0%; Pred. No. 2.7e-93;
iive 0; Mismatches 0;
ADD40788 standard; protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 43pp; German.
                                                                                                                                                                                                                                                polyps; hyperplasia; carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2002; 2002WO-EP014579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2001; 2001DE-01062556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALCE-) ALCEDO BIOTECH GMBH.
                                                                                  (first entry)
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                                                                                                                        Human HMGB1 protein.
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N-PSDB; ADD40787.
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Matches 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bullerdiek J;
                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                  15-JAN-2004
                                          ADD40788;
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the activity of CAP; (ix) as a biochip; (x) for diagnosing carcinoma; and or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as MAN vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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100.0%; Pred. No. 2.7e-93;
ive 0; Mismatches 0;
                                            215
                                                                                                                                                                                                               Cytostatic; carcinoma; lymphoma; cancer; human.
                                           SKKKKEEEEDEEDEEDEEEEEDEDEEEDDDDE
                                                        SKKKKEEEEDEEDEEDEEEEDEEDEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 1446; Opp; English.
                                                                                                                        ABM85677 standard; protein; 215 AA
                                                                                                                                                                                          Human protein sequence hCP43793.
                                                                                                                                                                                                                                                                                                                              01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                        28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY
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nes 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 215 AA;
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121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

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This invention relates to a novel vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytosis by microglia, which comprises a high mobility group protein 1 (HMG1), its partial peptide, or its salt. The invention may be useful for the production of compounds with a nootropic or neuroprotective activity acting as promoters of inhibition of amyloid beta 42 aggregation or promoters of amyloid beta 42 phagocytosis by microglia. The invention may also be useful for the production of a vaccine. The invention is useful for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy or preventing brain amyloidosis such as Alzeimer's disease. The present sequence is that of the protein encoded by the human high mobility group protein 1 (HMG1) gene which may be used during the creation of the novel
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vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis; microglia; high mobility group protein 1; HMG1; nootropic; neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy; brain amyloidosis; Alzheimer's disease; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytosis, useful for prophylaxis and/or treatment of Alzheimer's disease or Down's syndrome, comprises high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human high mobility group protein 1 (HMG1) protein SeqID2.
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100.0%; Pred. No. 2.7e-93;
iive 0; Mismatches 0;
                                                                                                                                               SKKKKEEEEDEEDEEDEEEEEDEEDEEEDDDE 215
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                                                                                                                                                                                                                                                                                                                                                  ADO60491 standard; protein; 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2004 (first entry)
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The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. The composition individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) that can be used to stimulate cytokine activity and increase immune response to assist in treating disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pharmaceutical composition comprises a polypeptide comprising an HMGB box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; vaccine; pharmaceutical composition; HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity.
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                                                                           SKKKKEEEEDEEDEEDEEEEEDEEDEEEDDDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES
                                                                                                                                                                                                                                                                                                                Human high mobility group box 1 (HMG1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1; 68pp; English.
                                                                                                                                                                                                        AD025918 standard; protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-2003; 2003WO-US036975.
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                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004046338-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                             26-AUG-2004
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B conspitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an artibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the playeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an useful in treating obesity and conditions characterised by activation of an early and a method of the collypeptide.
SIGDVAKKLGEMWINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                 121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obseity; inflammation; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; chronic is peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; aultiple sclerosis; cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                   Human high mobility group box 1 (HMGB1) protein #1.
                                                                                                                    SKKKKEEEEDEEDEEDEEDEEBEEEDEEDEEDEE 215
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                                                                                           SKKKKEEEEDEEDEEDEEEEEDEDEDEEEDDDDE
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                                                                                                                                                                                                                                                             ADO71477 standard; protein; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003; 2003WO-US037507.
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                                                                                                                                                                                                                                                                                                                                                         26-AUG-2004 (first entry)
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degeneration, arthritis, endometriosis, histiocytosis, psoriasis, rosacca, eruptive or cavernous haemangioma, tumours (especially melanoma, Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerorists and basal cell carcinoma), haemorrhoids, arteriosclerorists, angina pectoris, ischaemia, infarction, infarcility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing (including where associated with sunburn) and cardiac infarct, including cosmetic treatment, especially as a sun-protection composition. Compounds identified as modulators of the specified processes can also be used therapeutically. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGDVAKKIGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target; TAT; human, overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target (TAT) polypeptide PRO71096, SEQ:3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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   macular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 215;
   (proliferative) diabetic retinopathy, diabetic nephropathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1149; DB 8;
100.0%; Pred. No. 2.7e-93;
ive 0; Mismatches 0;
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Matches 215; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 215 AA;
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human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                             EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of nucleic acids encoding basic DNA-binding proteins, and their translation or transcription products, for treating diseases associated with e.g. anglogenesis, neovascularization or wound healing, also for
                                                                                                                                                                                                                                                                                                                        MCKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                          Gaps
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                                                                                                                                      Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic; ophthalmological; nephropathic; antiarthritic; antiinflammatory; cytostatic; gynaecological; antipsoriatic; dermatological; antiviral; vasotropic; antiarteriosolectic; cardiant; vulnerary; antiulcer; high mobility group protein;
                                                                                                                                                                                                          Indels
represents a human HMGB1 polypeptide of the invention
                                                                                                                                      100.0%; Score 1149; DB 8; 100.0%; Pred. No. 2.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKKKKEEEEDEEDEEDEEDEEDEEDEEDEEDDDE 215
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                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR45922 standard; protein; 215
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07-MAR-2003; 2003DE-01010160.
10-AUG-2003; 2003DE-01036642.
08-OCT-2003; 2003DE-01046614.
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                                                                                                                     Query Match
Best Local Similarity 100.
Matches 215; Conservative
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                                                                   Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004061456-A2
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide equences at least 80% identical to the TAT nucleic acids and polypeptide and polypeptide and polypeptide and polypeptide and polypeptide and enthods and compositions for the treatment or TAT polypeptide; and methods and compositions for the treatment or TAT polypeptide, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, pancreatic and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor; VEGF; vascular endothelial growth factor receptor; VEGFR; dermatological; edema; gene therapy; vulnerary; burn; skin cancer; cytostatic; wound healing; hematoma; pain; necrosis; ischemia, vasotropic; anglogenesis stimulation; vascularization; tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1149; DB 8; Length 215; 100.0%; Pred. No. 2.7e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                        Claim 12; SEQ ID NO 3888; 7273pp; English.
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Matches 215; Conservative
  prostate cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005011722-A2.
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The present invention relates to new vascular endothelial growth factor (VEGF) proteins useful for skin healing of a skin graft onto underlying tissue. The method involves contacting a skin graft flap or underlying tissue with an agent chosen from vascular endothelial growth factor C (VEGF-C) polynucleotides, vEGF-C polypeptides, VEGF-D polynucleotides, and vEGF-C polypeptides, VEGF-C polypeptides or reduce edema or increase perfusion at skin graft or flap. The composition comprises a gene therapy vector that encodes VEGF-C polynucleotide. The VEGF-C polypeptides or comprises the formula X-B-Z or Z-B-X, where X binds VEGF-C polypeptide comprises a heparin-binding amino acid sequence chosen from a prepro-VEGF-C sequence, and fragments that binds VEGF-3, where Z comprises a heparin-binding amino acid sequence, and B comprises a covalent attachment linking X to Z. The VEGF-D polypeptides, VEGF-C polypeptides, VEGF-D polymucleotides, and VEGF-D polypeptides, vEGF-C polypeptides, vEGF-D polymucleotides, and vEGF-D polypeptides, vEGF-C polypeptides, vEGF-D polymucleotides, and vEGF-D polypeptides, vEGF-C polymucleotides, vEGF-D polymucleotides, and vEGF-D polypeptides, vEGF-C polymucleotides, vEGF-D polymucleotides, 120 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180 SIGDVAKKIGEMWINTAADDKQPYEKKAAKIKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180 Improving healing of skin graft or skin flap to underlying tissue useful in mastopexy, cosmetic surgery, abdominoplasty, involves using composition of vascular endothelial growth factor-C or D polynucleotides 9 9 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKCHPDASVNFSEFSKKCSERWKTMSAKEKGKF 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF Gaps Asko-Seljavaara ö Length 215; Indels Tammela T, Query Match 100.0%; Score 1149; DB 9; Best Local Similarity 100.0%; Pred. No. 2.7e-93; Matches 215; Conservative 0; Mismatches 0; 181 SKKKKEEEEDEEDEEDEEBEEBEEDEEDEEDEDDDE 215 Example 11; SEQ ID NO 22; 119pp; English Karkkainen M, Ź ADX69343 standard; protein; 215 (LUDW-) LUDWIG INST CANCER RES 12-JUN-2003; 2003US-0478390P. 12-JUN-2003; 2003US-0478114P. Alitalo K, Saaristo A, Yla-Herttuala S, He Y; (LICN) LICENTIA LTD WPI; 2005-142834/15. and/or polypeptides Sequence 215 AA; 61 ADX69343; 181 ADX69343 SXXX В ò 요 a 셤 ઠ ઠે 8 Gaps

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ADY85326 standard; protein; 215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to heparin-binding vascular endothelial growth factor receptor 3 (VEGFR-3) proteins and encoding polymucleotides. The heparin binding VEGFR-3 proteins are used for stimulating lymphangiogenesis or angiogenesis in a mammal, and for modulating the growth of mammalian endothelial cells, mammalian endothelial precursor cells or hematopoietic progenitor cells. The polypeptide may also be used for promoting recruitment, proliferation, differentiation, migration or survival of neuronal cells or neuronal precursor cells, and for treating neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral Sclerosis (ALS), dementia, or cerebral palsy. The present sequence represents human amphoterin.
                                                                                                                                                                                                                                                                                                                                                                                                                                New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDMAKADKARYEREMKTYI PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKI KGEHPGL 120
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                                                  amphoterin; Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian; Anticonvulsant; VEGF-3 receptor; Angiogenesis stimulator; Gene Therapy; vascular endothelial growth factor receptor 3; VEGFR-3; angiogenesis disorder; neurodegenerative disorder; Alzheimers disease; Parkinsons disease; motor neuron disease; dementia; paralysis; VEGF-C; neurological disease; Huntingtons chorea; vascular endothelial growth factor receptor 3; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 63; 219pp; English.
                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                              12-JUN-2003; 2003US-0478390P. 23-SEP-2003; 2003US-00669176.
                                                                                                                                                                                                                                                                                  .2-JUN-2003; 2003US-0478114P.
                                                                                                                                                                                                                                                                                                                                                                              Tammela T;
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(first entry)
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Les 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 215 AA;
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05-MAY-2005
                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatcid arthritis. The present sequence represents a DNA encoding a PRO
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                                                                                                                                                                                                                            Antinflammatory, Immune disorder; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic; Hemosratic; Antianemic; Antithyroid; Antiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis.
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; Pred. No. 2.7e-93;
0; Mismatches 0;
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ADY14248 standard; protein; 215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 215; Conservative 0
                                                                                                                                                                        PRO polypeptide SEQ ID NO 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-2004; 2004WO-US026249.
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                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005016962-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                               05-MAY-2005
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High mobility group box, HMGB1; immune disorder; infection, immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; asthmatic; rheumation; asthma; rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                    Human high mobility group box protein HMGB1.
                                                                                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP.
(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                        Location/Qualifiers
                                                                                                                               32. 85
/label= A_box
                                                                                                                                                       /label= B_box
                                                                                                                                                                                                     10-SEP-2004; 2004WO-US029540.
                                                                                                                                                                                                                   10-SEP-2003; 2003US-0502349P
                      (first entry)
                                                                                                                                                .161
                                                                                                                                                                                                                                                          Warren HS, Tracey KJ;
                                                                                                                                                                                                                                                                        WPI; 2005-233421/24.
                                                                                                                                                                     WO2005025604-A2
                     02-JUN-2005
                                                                                                         Homo sapiens
                                                                                                                                                                                      24-MAR-2005
       ADY85326;
                                                                                                                                Region
                                                                                                                                                Region
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Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment

Claim 6; SEQ ID NO 1; 57pp; English.

The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB as 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-numan antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of protecting a subject against an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune to comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box.

Comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box.

A claimed method of treating an autoimmune disorder in an individual

comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate in an individual

comprises administering a HMGB polypeptide comprises administering a HMGB D box, or an immunosuppressive fragment or an immunosuppressive and immunosuppressive and immunosuppressive and immunosuppressive and immunosuppressive a fragment of these, and a vertebrate or non-naturally-occurring HMGB Ebox. The HMGB polypeptide is preferably a HMGB peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, psoritais or systemic lupus erythematosus (all claimed). The present sequence is that of the human HMGB protein, which can be used as the HMGB polypeptide in methods of the invention.

Sequence 215 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                                       61 EDMAKADKARYEREMKTY1PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides antibodies, or their antigen-binding fragments,
                                                                                      1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                       SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
                                                               1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            negals, antibacterial imminosuppressive, graft rejection, arthritis, antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiantiammacrory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; ischemia; vasotropic; Behcets disease; apatrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
                                     Gaps
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   Length 215;
                                   Indels
; Score 1149; DB 9;
; Pred. No. 2.7e-93;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 215; Conservative
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CC detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB A box but does not binding fragment) binds to a vertebrate HMGB A box but does not capecifically bind to non-A box epitopes of HMGB, and inhibits release of profein. A method of treating a condition characterized by activation of protein. A method of treating a condition characterized by activation of the invention, or its antigen-binding fragment. The condition is selected from a logarfat rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, gradically sepsis, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, and cachexia, especially sepsis, arthritis, or lupus. The present can dachexia, especially sepsis, arthritis, or lupus. The present can cachexia, especially sepsis, arthritis, or lupus. The present cachexia, especially sepsis, arthritis, or lupus.

XX Squence is also found in rat and mouse HMGB1.

Dhypoproper cachexia, especially sepsis, arthritis, or lupus.

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MATCHEST CONSETVATION OF $76-93;

MATCHEST CONSETVATION OF $76-93;

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Double Consetvente C
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SKKKKEREEDEEDEEDEEBEEDEEDEDEE 215

completed: April 6, 2006, 10:19:12 ne : 263.97 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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OM protein - protein search, using sw model

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6, 2006, 10:19:38 ; Search time 41.0197 Seconds (without alignments) 504.309 Million cell updates/sec

US-10-717-984-1 1149

1 MGKGDPKKPRGKMSSYAFFV......DEEBEEDEEDEDEDDDE Perfect score: Sequence:

215

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIËS

		Description	nonhistone chromos		nonhistone chromos	non-histone chromo	nonhistone chromos	nonhistone chromos	high mobility grou	nonhistone chromos	nonhistone chromos	high mobility grou	ίτγ	nonhistone chromos	nonhistone chromos	high-mobility-grou	high mobility grou	nonhistone chromos	nonhistone chromos	nonhistone chromos	HMG-1 - chicken	nonhistone chromos	gene HMG-T2 protei	nonhistone chromos	nonhistone chromos	dorsal switch prot	HMG1 protein - sea	protein F47D12.4 [HMG protein 1.2 -	protein F2D10.18 [high mobility grou
		01	S02826	S01947	NSRTH1	I48688	A28897	S29857	862355	NSHUH2	A34719	S54774	JC1114	JC1129	A27853	\$48708	T01071	S22359	S26062	\$30221	I50254	B61611	151067	A24019	820068	JC6179	JC4357	E88479	T43009	33	T03640
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ф	Query	Match	: 8	99.7	99.4	99.4	99.5	7.76	85.7	80.9	90.6	80.0	79.6	78.8	77.8	72.9	72.3	70.9	70.8	9.69	69.5	67.1	65.7	59.7	47.4	47.3	42.6	32.4	31.6	28.3	27.1
		Score	1149	1145	1142	1142	1140	1122.5		929	926.5	919	915	905	894	837.5	830.5	814.5	813.5	800	799	771	755	989	545	544	489	372	363	325.5	311
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ALIGNMENTS

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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: OL Dec.1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004
C.Accession: 802826; A33178; G33178
R.Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
R.Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
A.JTitle: A human placental cDNA clone that encodes nonhistone chromosomal protein HWG-1.
A.Reference number: 802826; MUID:89160247; PMID:2922262
                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S02826
A;Molecule type: mRNA
A;Molecule type: mIND: Whitehead, R.H.; Simpson, R.J.
B;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
B;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro
A;Reference number: A33178; MUID:91176935; PMID:2079031
nonhistone chromosomal protein HMG-1 - human
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A,Molecule type: protein
A,Residues: 2-13, XXF' <WAR>
A,Cross-references: UNIPARC:UPI00001771D7
A,Accession: G33178

A,Molecule type: protein A,Residues: 2-13,'XX',16-22 <WA2> A,Cross-references: UNIPARC:UP100001771D7

A; Gene: GDB: HMG1 C,Genetics:

A.Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DNA binding; nucleus F;6-83/Domain: HMG box homology <HMG1>
F;6-83/Domain: HMG box homology <HMG2>

ö Gaps ö Length 215; Indels Query Match 100.0%; Score 1149; DB 2; Best Local Similarity 100.0%; Pred. No. 9.2e-62; Matches 215; Conservative 0; Mismatches 0;

9 9 1 MCKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 셤 ð

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SKKKKEEEEDEEDEEDEEEEDEEDEEEEDDDDE 215 181

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NyAlternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C46771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
A;Title: 30-Kba heparin-binding protein of brain (amphoterin) involved in neurite outgrov
A;Reference number: A41175; MUID:91158468; PMID:1885601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A30188
A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC::UP1000173985
B;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvali Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced & A;Reference number: A48771; MUID:93374971; PMID:8366113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-10, R'. 12-82,84-95,97,'AS',100-215 <PAO>
A; Cross-references: UNIPARC:UP10000173984
R; Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A; Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 98-105, Xr. 107-112 < PA2>
A; Resperimental source: postnatal brain
A; Note: sequence extracted from NCBI backbone (NCBIP:137788)
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Reywords: chromosomal protein; DNA binding; nucleus
F; 2-15/Froduct: nonhistone chromosomal protein HMG-1 #status experimental
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                    nonhistone chromosomal protein HMG-1 - rat
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F;92-166/Domain: HMG box homology <HMG2>
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A, Molecule type: mRNA
A, Residues: 1-215 <MER>
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Ny Alternate names: 33K protein; high-mobility-group protein HMG-1

C.59ecies: Bos primigabilus tautus (cattle)

C.Date: 30.5ep-1989 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004

C.Accession: $01947; Asigli; $10959; 145910

C.Accession: $01947; Asigli; $10959; 145910

R.Kaplan, D.J.; Duncan, C.H.

Nucleic Acids Res. 16, 10375, 1988

A; Fittle: Rull length cDNA sequence for bovine high mobility group 1 (HMG1) protein.

A; Reference number: $01947; MUID:89057489; PMID:3194213

A; Residues: 1-215 < KAP>
A; Accession: $01947; MUID:89057489; PMID:3194213

A; Accession: $01947

A; Molecule type: mRWA

A; Residues: 1-215 < KAP>
A; Cooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.

R; Residues: 1-22, 264-270, 1980

A; Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.

A; Reserence number: Asisli; MUID:81138848; PMID:7202717

A; Molecule type: protein

A; Residues: 2-2, 2', 2', 24-40; 48-105, A', 107-157, X', 160-193, D', 195 < WAL>
A; Cross-references: UNIPARC:UP10000173987; UNIPARC:UP10000173988

R; Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.

FEBS: Lett. 267, 139-141, 1990

A; Mail Mail Mail Mail Midden Mail Midden Mail Mail Midden Mail Midden Mail Mail Midden Mail Mail Midden Mail Mail Mail Midden Mail Midden Mail Midden Mail Midden Mail Mail Midden Mail Mid
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A.Accession: $10959
A.Molecule type: protein
A.Residues: 2-22, X', 24-38 «CHR»
A.Residues: 2-22, X', 24-38 «CHR»
A.Residues: 1-22, X', 24-38 «CHR»
A.Friche: Dixon, G.H.
B.T.; Dixon, G.H.
A.Frithe: Isolation and partial sequence of bovine cDNA clones for the high-mobility-grou A.Reference number: 145910; MUID: 84128872; PMID: 6141822
A.Accession: 145910
A.Accession: 145910
A.Residues: YegG', 119, V', 121-215 «PEN»
A.Residues: YegG', 119, V', 121-215 «PEN»
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F; 2-315 Pionuct: nonhistone chromosomal protein HMG-1 #status predicted 
F; 2-315 Pionuct: HMG box homology 
F; 2-316 Pionuct: HMG box homology 
F; 2-316 Pionuct: HMG box homology 
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181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEEDDDDE 215
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Gaps

us-10-717-984-1.rpr

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A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI
A;VOSs-references: UNIPARC:Translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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high mobility group protein 1 - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Spate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
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R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: $29857; MUID:93176821; PMID:8439568
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DNA binding; nucleus F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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Pred. No. 3.5e-60;
0; Mismatches 2;
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                                                                                                                                             DB 2;
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                                                                                                                                          99.2%; Score 1140; DB 2;
llarity 99.1%; Pred. No. 3.2e-61;
Conservative 1; Mismatches 1
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nes 213; Conservative
                                                                                                                                                                    Best Local Similarity
Matches 213; Conserv
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C;Species: Sus scrofa domestic pig)
C;Species: Sus scrofa domestic pig)
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequentance number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
A;Molecule type: mRNA
A;Residues: 1-215 < 475U>
A;Cosserences: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:916
                                                                                                                                                                 A; Tele: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc A; Reference number: 148687; MUID:92335012; PMID:1630928
A; Reference number: 148688
A; Recession: 148688
A; Retarus: preliminary; translated from GB/EMBL/DDBJ
A; Roleoule type: mRNA
A; Residues: 1-215 < RES>
A; Cross-references: UNIPROT:P07155; UNIPARC:UP10000008A6; EMBL:Z11997; NID:g53381; PIDN R; PFPrarari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A; Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A; Reference number: A55402; MUID:95050689; PMID:7961836
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R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
RMamn. Genome 5, 91-99, 1994
A;Title: Molecular cloning expression analysis, and chromosomal localization of mouse H
A;Reference number: I57021; MUID:94235965; PMID:8180479
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A;Cross-references: UNIPARC:UP100000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
C;Genetics:
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  non-histone chromosomal high-mobility group 1 protein - mouse C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Accession: 148688; A55402; T57021
R;Yotov, W.V.; &L-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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Pred. No. 2.4e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
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Best Local Similarity 99.1
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A55402
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high mobility group 2 protein - mouse
C.Species: Mus musculus (house mouse)
C.Species: An musculus (house mouse)
C.Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C.Accession: S54774; S52211

EMBO J. 14, 1198-1208, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A.Title: High mobility group protein 2 functionally interacts with the POU domains of oct.
A.Reference number: S54774
A.Recession: S54774
A.Recession: S54774
A.Recent by preliminary; nucleic acid sequence not shown
A.Relaus: preliminary; nucleic acid sequence not shown
A.Residues: 1-210 <2WI>
A.Residues: 1-210 <2WI
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
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NSHUH2

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C.Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Date: Structure of a gane coding for human HMG2 protein.

A;Feference number: A42425; MUID:92202209; PMID:1551873

A;Residues: 2-209 cSHI>
A;Residues: 1-209 
C; Accession: S62355
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
BMBO J. 15, 548-561, 1996
A.Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in A;Reference number: S62355, MUD:96174815; PMID:8599938
A;Accession: S62355
A;Accession: S623
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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AKKKEEEDED----DDEEEDBEEDEEEEEDDDDE 210
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C,Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Richemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nuclec A;Reference number: A34719; MUID:90275208; PMID:2350545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:A;CySuperfamily: nonhistone chromosomal protein HMG-2; HMG box homology chiding; nucleus
F;6-83/Domain: HMG box homology chidis
F;92-166/Domain: HMG box homology cHMG2>
                                                                                                                                                                EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGKGDPNKPRGKMSYAFFVQTCREEHKKKAPDSSVNFAEFSKKCSERWKTMSAKEKSKF
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A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Recession: JC1129
A;Molecule type: mRNA
A;Residues: 1-207 <SPA>
A;Coss-references: UNIPROT:P26584; UNIPARC:UPI0000171348; GB:M80574; NID:g211928; PIDN: C;Superfamily: nonhistone chromosomal protein HNG-2; HMG box homology C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiLee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H. Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKSKSDAGKKGPGRPAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGKGDPNKPRGKMSSYAYFVQTCPREHKKKHPDSSVNFAEFSRKCSERWKTMSSKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEEDEEDEEDEEDDDDE
                                                                                                                                                                                                                                                                                                                                                  2; Length 207;
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98.8%; Pred. No. 1e-46;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: mRNA
A.Residues: 1-170 c.LES-
A.F.Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C.Superfamily: nonhistone chromosomal protein HMG-2; HMG k
C.F.Swyords: chromosomal protein; DNA binding; nucleus
F.F.SS/Domain: HMG box homology (fragment) cHMG1>
F;47-121/Domain: HMG box homology cHMG2>
                                                                                                                                                                                                                                                                                                                                               ; Score 905; DB 2;
; Pred. No. 2.8e-47;
18; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKKAEPEEEEEEEDEEEEEEEEE 207
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high-mobility-group-1 protein - trout
                                                                                                                                                                                                                                                                                                                                                  78.8%;
80.2%;
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Best Local Similarity 98.8<sup>§</sup>
Matches 168; Conservative
  R, Sparrow, D.B.; Wells, J.R.E.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                        Gene 114, 289-290, 1992
A, Title: Sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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high-mobility group protein 2 - chicken
high-mobility group protein 2 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: O9-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1114
R;Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
A;Accession: JC1114
A;Molecule type: mRNA
A;Residues: 1-207 - CDAV-
A;Residues: 1-207 - CDAV-
A;Cosmant: The high mobility group proteins are among the most abundant nonhistone chrom
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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NiAlternate names: high-mobility-group protein 2
C;Species: Gallus gallus (chicken)
C;Date: 05-Mar.1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
C;Accession: JC1129
                                                                                                                                                                                                                                                     1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNPAEFSKKCSERWKTMSAKEKSKF
                                                                                                                                                                                                                    1 MGKGDPKKPRGKMSSYAFFVOTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                        Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 915; DB 2; Length 20
81.2%; Pred. No. 7e-48;
ive 17; Mismatches 22; Indels
                                                                                                                                                            21; Indels
                                                                                                        Query Match 80.0%; Score 919; DB 2; Best Local Similarity 80.5%; Pred. No. 4.1e-48; Matches 169; Conservative 20; Mismatches 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: DNA binding; nucleus P; 6-83/Domain: HMG box homolomy
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Search completed: April Job time: 42.0197 secs
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NyAlternate names: HMG-T protein T - rainbow trout
NyAlternate names: HMG-T protein
Cippecies: Oncortynchus mykiss (rainbow trout)
Cippecies: Oncortynchus mykiss (rainbow trout)
Cipate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Cipate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Cipate: 12-Feb-1999 #sequence of CDNA clones coding for a member of the family of high Nucleic Acids Res. 13, 4871-4888, 1988
Nucleic Acids Res. 13, 4871-4888, 1988
Airtle: Isolation and sequence of CDNA clones coding for a member of the family of high Airtle: Isolation and sequence of CDNA clones coding for a member of the family of high Airtle: Isolation and sequence of CDNA clones coding for a member of the family of high Airtle: Isolation ary; translated from GB/EMBL/DDBJ
Airtle: Lyone: mRNA
Airtle: NULL of SPENDA
Cisuperfemily: nonhistone chromosomal protein HMG-2; HMG box homology
F;91-165/Domain: HMG box homology < HMG>
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72.9%; Score 837.5; DB 2; Length 204;
Best Local Similarity 71.8%; Pred. No. 2.8e-43;
Matches 150; Conservative 34; Mismatches 20; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.3%; Score 830.5; DB 2; Length 204; Best Local Similarity 71.3%; Pred. No. 7.3e-43; Matches 149; Conservative 35; Mismatches 20; Indels 5
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OM protein - protein search, using sw model

Run on:

April 6, 2006, 10:13:48; Search time 253.898 Seconds (without alignments) 597.439 Million cell updates/sec

Title: Perfect score:

US-10-717-984-1 1149 1 MGKGDPKKPRGKMSSYAFFV......DEEBEEDEEDEDEBEEDDDDE 215

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	homo sa	macac	spalax					'5 m high mobi	bos tau	spal	2 spalax leuc		9 rattus norv	2 mus musculu	2 sus scrofa	1 homo sapien		_	gall	homo	homo	homo	xenop	xeno	1 mus musculu	6 xenopus lae	xenc	BUM	4 mus musculu	_	2 homo sapien
	esci	25t7c3	Q4r844	09qx40	Q6yka4	P09429	99Wy	548r	Q58ev5	P10103	088611	088612	P63158	P63159	Q6p202	1268	014321	9bq0	09yh06	09puk9	Q9nqj4	09ugv6	Q5t7c5	Q6p4n5	Q78242	Q5bkq1	091596	Qegnq5	Q8bnm0	Q8c7c4	P07156	05u072
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SUMMARIES		QST7C3 HUMAN	Q4R844 MACFA	40 SPAEH	CANFA	HMG1 HUMAN	Y6_SPAEH	R9_RAT	Q58EV5_MOUSE	BOVIN	088611_SPAEH	088612_SPAEH	HMG1 MOUSE	RAT	02 MOUSE	PIG	Q14321_HUMAN	02 MOUSE	06_CHICK	K9_CHICK	J4 HUMAN	HMG1X_HUMAN	CS_HUMAN	NS_XENTR	42_XENLA	Q5BKQ1_MOUSE	091596_XENLA	OS XENLA	D8BNW0_MOUSE	Q8C7C4_MOUSE	HMG1_CRIGR	25U072_HUMAN
נט	£	QST7	Q4R8	090X	HMG1	HMG1	MO60	0548	058E	HMG1	0886	9880	HMG1	HMG1	Q6P2	HMG1	0143	08B 0	09YH	O9PU	ON60	HMG1	Q5T7	Q6P4	0752	O5BK	0915	OCCINOS	Q8BN	Q8C7	HMG1	OSO
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de	Query Match	100.0	100.0	99.7	99.6	9.66	99.4	99.4	6	σ	99.1	99.0	99.0			98.8	98.3		92.9		92.3	91.4	89.2	87.5	87.1	86.7	85.7	85.4	84.3	83.1	82.5	80.9
	Score	1149	1149	1145	1144	1144	1142	1142	1142	1140	1139	1138	1137	1137	1136	1135	1129	1125	1067	1061.5	1061	1050.5	1025	1005	1001	966	984.5	981.5	696	955	948	929
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04R844 MACFA PRELIMINARY; PRT; 215 AA.
04R8447 MACFA PRELIMINARY; Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QtsA-13487, similar to human high-mobility group

RESULT 2 04R844 MACFA ID 04R844 MAC AC 04R844; DT 13-SEP-20 DT 13-SEP-20 DT 13-SEP-20 DT Testis CD DE Testis CD

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P26583 P17741 Q5u071 Q5fvp0 P30681 P526584 Q6avu3 Q75mm1	265789 265789 265786 291764			ta; Buteleostomi; Catarrhini; Hominidae;		ases.	DNA-dependent; CRC64;	Length 215, Indels (KKCSERWKTN	KKCSERWKTN	FLFCSEYRPE	FLFCSEYRPE
		AA.	ed) sequence update) annotation update)			DBJ databases	ion, DNA-de 417B5 CRC64	DB 2; 9e-59; 0;	MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF	MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF	EDWAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL	EDMAKADKARYEREMKTYI PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL
HMG2 HUMAN HMG2 PIG Q5UG71 HUMAN Q5FVP0 RAT HMG2 MQUSE HMG2 GHICK Q8AVU3 XENLA Q75MM1 HUMAN	V/2/Co_brane Q6/7/95 SENTR Q6/0X/86_BRARE Q91764_XENLA ALIGNMENTS	215	ed) sequence update) annotation updat	4 ; D		EMBL/GenBank/DDBJ -; Genomic_DNA. IEA. EA.	<pre>// IEA. of transcription, 8A868CF277D417B5</pre>	ore 1149; DB ed. No. 6.9e- Mismatches	SEHKKKHPD	SEHKKKHPD	TXKKFKDPN	rKKKFKDPN
HMG2_HUMAN HMG2_PIG O5U071_HUM O5U071_HUM O5U072_MOUSE HMG2_RAT HMG2_RAT OBAG3_XEM O7SW11_HUM	Q6 P7 W Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	PRT;	t)	=RP11-550P23.1-00 Chordata; Craniat Euarchontoglires;		EMBL/C; -; Ger i : EA. IEA.	F:DNA binding; IEA. P:regulation of tra A; 24894 MW; 8A86	So. Pr	FVQTCRI	FVQTCRI	IPPKGET	IPPKGET
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Le K.-1.D., Lum H.-K., Nevo E.;
Le K.-1.D., Lum H.-K., Nevo E.;
Le Submitted (AUG-1999) to the EMEL/GenBank/DDBJ databases.

EMBL; AF078820; AAC27653.2; -; Genomic_DNA.

R HSSP; P07156; LNHN.

R GO; GO:00005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005635; F:DNA binding; IEA.

R GO; GO:0005635; F:DNA binding; IEA.

R GO; GO:0000563; Highmoblty_12.

R InterPro; IPR00013; Highmoblty_12.

R Pfam; PF00056; HMG dox; Z.

R Pfam; PF00056; HMG dox; Z.

R PRANTS; RN00398; HMG; 2.
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                                                                                                                                                                                                                                                                                                                                                                                       MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                             International consortium for macaque cDNA sequencing, analysis; "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications."; submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
box 1 (HWGB1),...
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecides, Cercopithecinae; Macaca.
                                                                                                                                                                                                       Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; Subaritution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (NAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AB166615; BAE00728.1; -; RNA. SAB168615; AA; 24894 MW; 8A868CF277D417B5 CRC64;
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                                                                                                                                                                                                                                                                                                            100.0%; Score 1149; DB 2; Length 215; 100.0%; Pred. No. 6.9e-59; tive 0; Mismatches 0; Indels 0.
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Last annotation update)
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NCBI_TaxID=30637;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bullerdies J., Nolte I.;
Bullerdies J., Nolte I.;
Bullerdies J., Nolte I.;
Wolecular characterization of the canine HWGB1.";
Cytogenet. Genome Res. 101:33-38(2003).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA (By similarity).
-!- SUBCELULAR LOCATION: Noticer (By similarity).
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last senotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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MEDLINE=22912580; PubMed=14571134; DOI=10.1159/000073415;
Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
                                                                                                                                      Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS00183; HMG BOX 2; 2.
Chromosomal protein; DNA-Dinding; Nuclear protein; Repeat.
INIT_MET 0 0 By similarity.
                                                                                                                                                                                                     Indels
; PS00353; HMG_BOX_1; 1.
; PS50118; HMG_BOX_2; 2.
E 215 AA; 24895 MW; 599FBBA6FDF41F17 CRC64;
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                                                                                                                               Score 1145; DB 2;
Pred. No. 1.2e-58;
1; Mismatches 0;
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EMBL; AY135521; AAN1319.1; -; Genomic_DNA.

HSSP; P07155; 1AAB.

ENS, QGYKA4; 1-83, 92-170.

Ensembl; ENSCAFG0000006597; Canis familiaris.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000910; HMG_12_box.

InterPro; IPR000910; HMG_12_box.
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                                                                                                                                      99.78;
                                                                                                                               Query Match
Best Local Similarity 99.5
Matches 214; Conservative
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                       1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
"Cloning of human full open reading frames in Gateway(TM) system entry
                                                                                            2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                     DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS
                                                                         Gaps
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
                                                                                                                                                                                                                                                                                               HWG1 HUMAN STANDARD; PRT; 214 AA. P09429; QG1BE1; 01-MAR-11999 (Rel. 10, Created) 01-AWG-1990 (Rel. 15, Last sequence update) 113-SEP-2005 (Rel. 48, Last annotation update) High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
PErrari S., Finelli P., Rocchi M., Bianchi M.E.;
"The active gene that encodes human high mobility group 1 protein (HMG1) conteains introns and maps to chromosome 13.";
Genomics 35:367-371(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89160247; PubMed-2922262;
Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal
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                                                   Score 1144; DB 1; Length 214; Pred. No. 1.3e-58;
                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA].
He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhc
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The German cDNA consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
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8 78 HMG box 1.
94 162 HMG box 2.
185 214 AB/D10-rich (acidic).
214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;
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                                            99.6%; Scott 100.0%; Pred. No. 1... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein HMG-1.";
Nucleic Acids Res. 17:1197-1214(1989)
                                                                                                                                                                                                                                                                                                                                                                       Name=HMGB1; Synonyms=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA]
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                     214;
          DNA_BIND
COMPBIAS
SEQUENCE
                                                                                                                                     62
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 DNA_BIND
                                                    Query Match
                                                               Local
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                                                                       Matches
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TISSUB-ERRIAN, Cervix, and Testis;

NUCLECOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUB-Errian, Cervix, and Testis;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Raugner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zebeberg B., Buetow K.H., Schaefer C.F., Bhara N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raba S.S., McZwan P.J., McKerran R.J., Malek J.A., Gunazatne P.H.,

Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Mammary carcinoma;
MEDLINE=97295304; PubMed=9150946;
RESEMINE=97295304; PubMed=9150946;
Stammussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
Simpson R.J., Dorow D.S.;
Simpson R.J., Dorow D.S.;
"Two-dimensiolanal electrophoretic analysis of human breast carcinoma
procteins: mapping of proteins that bind to the SH3 domain of mixed
lineage kinase MLK2.";
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
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                                            Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophoresis 18:588-598 (1997).
-!- FUNCTION: Binds preferentially single-stranded DNA and double stranded DNA.
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P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-366083;
O15350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606;
-!- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                                                                                        Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases
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EMBL; U51677; AAB08987.1; -; Genomic_DNA.
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Ensembl; ENSG0000189403; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 57-64 AND 112-126.
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CR749614; CAH18408.1; -; MENA.
CR456863; CAG33144.1; -; MENA.
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BT020159, AAV38861.1, -; mRNA.
BC003378, AAH0378.1; -; mRNA.
BC030981, AAH30981.1; -; mRNA.
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SMR; P09429, 1-83, 92-170.
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H-InvDB; HIX0011209; -.
MIM; 163905; -.
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InterPro; IPR000910; HMG_12_box.
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                                                                                                                                                                                                                                                                                                GKGDPKKPRGKMSSYAPPVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKPE
                                                                                                                                                                                                                                                                                      GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Spalacinae; Nannospalax.
                                                                                                                                                                                                                                                                    Gaps
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR078819; AAC27652.1; -; Genomic_DNA.
HSSP, P07156; INHN.
SMR; O90W76; 2-84, 93-171.
GO; GO:00005785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; P:DNA binding; IEA.
GO; GO:0006535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
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                                                                                                                                                                                                                                                 99.6%; Score 1144; DB 1; Length 214; 100.0%; Pred. No. 1.3e-58; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                       -> D (in Ref. 5).
B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                           HMG box 1.

HMG box 2.

Asp/Glu-rich (acidic).

E -> D (in Ref. 5).
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Last annotation update)
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                                                                                                                                                                                                                                24763 MW;
                                                                                                                                                                       Nuclear protein; Repeat.
INIT MET 0 0 0
DNA BIND 94 162
COMPEIAS 185 214
SEQUENCE 214 AA; 24763
                                                                                                                                                                                                                                                 Query Match 99.6
Best Local Similarity 100.
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
"Amphoterin is associated with the development of the kidney.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR275734; AAR82799.1; -: mRNA.
SEQUENCE 215 AA; 24894 MW; 8A868DBZ66D552B5 CRC64;
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                                                                                                                                                                                                    99.4%; Score 1142; DB 2; Length 215; 99.5%; Pred. No. 1.8e-58; ive 0; Mismatches 1; Indels
                                                                               PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Pfam; PF00505; HMG box; Z. PRINTS; PR00886; HIGHMOBLTY12. SMART; SMO0398; HMG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                   Best Local Similarity 99.5
Matches 214; Conservative
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Q548R9 RAT PRELIMINARY;
Q548R9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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STRAIN=FVBN/N; TISSUE=Colon, and Mammary tumor. C3;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KETAUSPETG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bratchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahety J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rottiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                         10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
High mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-length enriched library, Clone:Al30064Kll product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-2105560; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=2105660; PubMed=11217851; DOI=10.1038/35055500; Medline 21. Shindsawa A., Shibara K., Ishingawa A., Fukunishi Y., Koohino M., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Flestschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/60; TISSUE=Heart, and Thymus; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hitch-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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                 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FVB/N; TISSUE=Mammary tumor. C3;
                                              Created)
                                                                                                                                                        box 1, full insert sequence).
                                            10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Colon;
                 OSBEVS MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
                                                                                                                                                                                                                                 Muridae; Murinae; Mus.
                                                                                                                                                                                    Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGC Project;
                                                                                                                                                                    Name=Hmgbl;
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Distriction S. Hill D., Machiman M., Hube D.M., Kandya M., Lee N.H., Ordens P., Mill D., Machiman M., Hube D.M., Kandya M., Archimonia B., Kingwald M., Marzarchii J., Womberte P., M. Stork K., Sator K., Schoenbach G., Saya T., Shibata Y., Stork K., Sator K., Storkenbach M., Machiman J., Marzarchii J., Manhaderia M., Sator K., Sator K., Storkenbach G., Saya T., Shibata Y., Stork K., Sator K., Shibata Y., Sator K., Storkenbach G., Saya T., Shibata Y., Stork K., Sator K., Manhada M., Manhada M., Manhada M., Maranga M., Manhada M.,
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RACEGOTIOE SEQUENCE.

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rududa S., Puruno M., Hanagaki T., Hara A., Hashizume W., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Rududa S., Puruno M., Hanagaki T., Haraoka T., Hirozane T., Hayashida K., Imotani K., Ishii Y., Iltoh M., Kagawa I., Kauwawa T., RA Kachi H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Kawai J., Kojima Y., Konno H., Rouda M., Koya S., Ruzito R., Saitoh H., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Sasaki D., Shibata K., Yakau-Akahira S., Takeda Y., Tanaka T., Radashi D., Shibata K., Yakau-Akahira S., Takeda Y., Tanaka T., Radamura C., Sakai K., Sakai C., Sakai K., Sakai C., Sakai C., Sakai C., Sakai K., Sano H., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

B. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

B. RMBL, RC091741, BAH9174111; -; mRNA.

B. RMBL, RC091741, BAC3920921; -; mRNA.

B. RMBL, RC091741, BAC3920921; -; mRNA.

B. RMBL, RC091741, Hagbl.

B. RMBL, RC091741, Hagbl.

B. RMBL, RC091741, Hagbl.

B. RMBL, RC091741, Hagbl.

B. RMBL, RC09109191, Hmgbl.

B. RMBL, RC09109101, Hmgbl.

B. RMBL, RC09109101, HMG 12 box.

B. RMTT, SN000861, HIGHMBLYT12.

B. RMTT, SN00986; HIGHMBLYT12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takahu-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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PROSITE; PS50118; HWG BOX 2; 2.
SEQUENCE 215 AA; 24894 MW; 8A868DE266D552B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKKKKEEEEDEEDEEDEEDEEEDEEEDDDDE 215
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Matches 213; Conservative
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ID HMG1_BOV
AC P10103;
DT 01-MAR-1
DT 13-SEP-2
DE High mob
       RAPARA RA
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE-B113848; Pubmeda-7202717; DOI-310.1016/014-5793 (80) 80453-4;
Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
"The primary structures of non-histone chromosomal proteins HWG 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITAL 90306387, PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; "High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not to other types of Z-DNA."; PEBS Lett. 267:139-141(1990).

-I. FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.

-I. SUBCELLULAR DOCATION: Nuclear.

-I. SIMILARITY: Belongs to the HMG1/HMG2 protein family.

-I. SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                MEDLINE=84128872; PubMed=6141822;
Pentecost B., Dixon G.H.;
"Isolation and partial sequence of bovine cDNA clones for the high-mobility-group protein (HMG-1).";
Biosci. Rep. 4:49-57(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMR; P10103; 1-83, 92-170.

R GO; GO: 0000793; C: condensed chromosome; ISS.

R GO; GO: 0000793; C: condensed chromosome; ISS.

R GO; GO: 0000518; F: protein binding; ISS.

R GO; GO: 0006218; P: protein binding; ISS.

R GO; GO: 0006219; P: DNA repair, DNA ligation; ISS.

R GO; GO: 0006219; P: DNA repair, DNA ligation; ISS.

R GO; GO: 0006221; P: DNA repair, DNA ligation; ISS.

R GO; GO: 0006225; P: establishment and/or maintenance of chromat. . .; GO; GO: 0006325; P: establishment and/or maintenance of chromat. . .; GO; GO: 01055; P: establishment and/or maintenance of chromat. . .; R GO; GO: 01055; P: establishment and/or maintenance of chromat. . .; R GO; GO: 01055; P: establishment and/or maintenance of chromat. . .; R GO; GO: 0106505; P: establishment and/or maintenance of chromat. . .; R Pfam; PF00505; PR00910; PMG 12 box.
                                                                                                                                                                 STRAIN=Holstein; TISSUB=Fetal thymus;
BRDILNES-8957488; PubMed=1194213;
Kaplan D.J., Duncan C.H.
"Full length cDNA sequence for bovine high mobility group 1 (HMG1)
                          Bos faurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0086, HGHWOBLTY12.
SWART, SM00398, HMG; 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
Chromosowal protein; Direct protein sequencing; DNA-binding;
                                                                                                                                                                                                                                                                           Nucleic Acids Res. 16:10375-10375(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMG box 1.
                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X12796; CAA31284.1; -; mRNA.
EMBL; M26110; AAA30567.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 122:264-270(1980).
                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA]
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INIT MET 0 0 0
DNA_BIND 8 78
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HSSP; P07156; 1NHN.
                   Bos taurus (Bovine)
                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                       protein.
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SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                      SIGDVAKKLGEMANNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LE K.-L.D., Lum H.-K., Nevo E.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078818, AAC27651.1; -; Genomic_DNA.
HSSP; P07156; 1NHN.
R RSP; P07156; 1NHN.
R GO; GO:0000785; C:chromatin; IEA.
GO; GO:00005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
R GO; GO:000135; Highmoblty 12.
R InterPro; IPR000135; Highmoblty 12.
R InterPro; IPR00086; HiGHMOBLY 12.
R Pfam; PR00086; HGHMOBLY 12.
R PRINTS; RR00886; HGHMOBLY 12.
R R Pfam; PR00086; HGHMOBLY 12.
R R PART; SN00886; HGHMOBLY 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Spalacinae, Nannospalax.
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P63158; POT155; P27109; P27428;
01.4RP-1988 (Rel. 07, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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SEQUENCE 215 AA; 24923 MW; 1C6FB6845CA1E6C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
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98.6%; Pred. No. 3e-58;
ive 3; Mismatches
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                                                                                                                                                                                                                                                                                                      215 AA
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                                                                                                                                                                                                                                                                                                 O88612 SPAEH PRELIMINARY;
088612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.6
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=HMG1;
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HMG1_MOUSE
ID HMG1 M
AC P63158
DT 01-APR
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DE H1GP M
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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GO; GO:0000785; C:chromatin; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; E:nucleus; IEA.

GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000135; Highmobity_12.

InterPro; IPR000135; HMG_12_box.
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                                                                                                                                                                                                 99.2%; Score 1140; DB 1; Length 214; 99.5%; Pred. No. 2.3e-58; rive 1; Mismatches 0; Indels
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                         Asp/Glu-rich (acidic).

C -> S (in Ref. 3).

C -> A (in Ref. 3).

EFPGL -> PGGGV (in Ref. 2).

E -> D (in Ref. 3).

K -> D (in Ref. 3).
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO78817; AAC27650.2; -; Genomic_DNA.
HSSP; P07156; 1NHN.
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SEQUENCE 215 AA; 24905 MW; 64816B6FCF6033EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
High mobility group protein.
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NCBI_TaxID=30637;
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PRINTS; PR00886; HTGHMOBLTY12.
SMART; SM00398; HMG; 2.
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088611;
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Matches 213; Conservative
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DNA BIND
COMPBIAS
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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U00431; AAA20508.1; -; mRNA
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78
162
214
178
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DNA BIND
DNA BIND
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EMBL;
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MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUBDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHORL S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K.M., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Manna M.A., Schein J.E., Jones S.J.M., Marra M.A.;

"Manna M.A., Rodriguez M.D., Manna M.A., Schein J.E., Jones S.J.M., Marra M.A.;

"Manna M.A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.

MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hmgl-containing sequences.";
Manm. Genome 5:91-99(1994).
                           Mus musculus (Mouse).
Bukaryota, Matazao, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/Sv; TISSUE=Liver;
MEDLINE=55050689; PubMed=7961836;
MEDLINE=55050689; PubMed=7961836;
MEDLINE=5. Ronfandi L., Calogero S., Bianchi M.;
"The mouse gene coding for high mobility group 1 protein (HMG1).";
J. Biol. Chem. 269:28803-28808(1994).
                                                                                                                                                                                                       STRAIN=C3H/He;
MEDLINE=92335012; PubMed=1630928;
Yotov W.V., St Arnaud R.;
"Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group protein-1 (HMG1).";
Nucleic Acids Res. 20:3516-3516 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the HMG1/HMG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghosh B.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
  Name=Hmgbl; Synonyms=Hmg-1, Hmgl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                            NCBI_TaxID=10090;
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EMBL; Z11997; CAA78042.1; -; mRNA.

removed

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121
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P63159; P07155; P27109; P27428;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HWG-1) (High mobility group protein 1 (MMG-1) (High mobility group protein 1 (Reparin-binding protein p30).
Name-Hmgbl; Synonyms-Hmg-1, Hmgl;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00153; HMG BOX 1; 1.
PROSITE; PSS0118; HMG BOX 2; 2.
Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurogna
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                  SMR; P63158; 1-83, 92-170.
MGI; MGI: 96113; Hmgbl.
GO; GO:0005613; C:extracellular space; IDA.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0010235; F:nitric-oxide synthase regulator activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
GO; GO:0006810; P:transport; IDA.
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E -> V (in Ref. 4).
D -> E (in Ref. 3).
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
HMG box 1.
HMG box 2.
EMBL; X80457; CAA56611.1; -; Genomic_DNA.
EMBL; L38477; AAA57042.1; -; mRNA.
EMBL; BCO0656; AAH06586.1; -; mRNA.
EMBL; BCO08565; AAH08565.1; -; mRNA.
EMBL; BCO08509; AAH08505.1; -; mRNA.
EMBL; BCO83009; AAH83067.1; -; mRNA.
FNBL; L48688; 148688.
SMR; P631189; 1483, 92-170.
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MEDLINE=88067717; PubMed=3684582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR000135; Highmoblty 12.
InterPro, IPR000910; HMG 12 box.
Pfam; PF00505; HMG box; 2.
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SMR; P63159; 1-83, 92-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                              "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the extension of neurite-type cytoplasmic processes in developing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spectroscopy.";
Biochemistry 34:16596-16607(1995).
allochemistry 34:16596-16607(1995).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
-!- function that has a role in double stranded DNA. Heparin-binding protein that has a role in double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material. SIMILARITY: Belongs to the HMG1/HMG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley;
MEDLINE-96118376; PubMed-8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue E.D.;
"Structure of the A-domain of HMG1 and its interaction with DNA as
studied by heteronuclear three- and four-dimensional NMR
                                                                                                                                             MEDLINE=91358468; PubMed=1885601;
Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala "30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgrowth. Amino acid sequence and localization in the filopodia of the advancing plasma membrane.";
J. Biol. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 87-164.
MEDINE=93233672; PubMed=8467791;
MEDINE=9323672; PubMed=8467791;
Thomas J.O.;
Thomas J.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the HMG box motif in the B-domain of HMG1."; EMBO J. 12:1311-1319(1993).
                                                                                    Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUBE-Kidney, Prostate, and Testis;
NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                  NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE
Paonessa G., Frank R., Cortese R.; "Nucleotide sequence of rat liver HMG1 cDNA."; Nucleic Acids Res. 15:9077-9077(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M64986; AAA40729.1; -; mRNA.
EMBL; Y00463; CAA68526.1; -; mRNA.
EMBL; BC061779; AAH61179.1; -; mRNA.
EMBL; BC081839; AAH81839.1; -; mRNA.
EMBL; BC088402; AAH88402.1; -; mRNA.
PIR; A41175; NSRTH1.
PDB; IAAB; NMR; @=183.
PDB; ICKT; X-ray; A=7-77.
PDB; IHME; NMR; @=88-164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell Biol. 107:2293-2305(1988).
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                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 1-20
                                                                   SEQUENCE REVISION
                                                                                                                                                                                                                                                                                                                                                                                                 Panula P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurons.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                            PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
3D-structure; Chromosomal protein; Direct protein sequencing;
DNA-binding; Heparin-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%; Score 1137; DB 1; Length 214; 99.1%; Pred. No. 3.4e-58; ive 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24763 MW; B3C6A91FD6F1B133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                       HMG box 1.
HMG box 2.
Asp/Glu-rich (acidic)
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                                InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12_box.
Pfam; PP00505; HMG box; Z.
PRINTS; PR00886; HIGHMOBLTY12.
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Q6P202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 99.1
hes 212; Conservative
                                                                                                           SMART; SM00398; HMG; 2.
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                 RGD; 2802; Hmgb]
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185
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DNA BIND
DNA BIND
COMPBIAS
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Woren B.D., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BC064790; AAM64790.1; -; mRNA.

REMBL, BC064790; AAM64790.1; -; mRNA.

RISP; P07155; 1AAB.

RISP; P07155; 1AAB.

RISP; P07155; 1AAB.

ROG; P070005613; C:extracellular space; IDA.

ROG; P070005613; F:nitric-oxide synthase regulator activity; IDA.

ROG; P070006810; P:nitric-oxide synthase regulator activity; IDA.

ROG; P070006810; P:nitric-oxide biosynthesis; IDA.

ROG; P07006810; P:nitric-oxide biosynthesis; IDA.

ROG; P070006810; P:nitric-oxide biosynthesis; IDA.
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13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 98.9%; Score 1136; DB 2; Best Local Similarity 98.6%; Pred. No. 3.9e-58; Matches 212; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SKKKKEBEDDEEDEEDEEEEBEBDBDBB 215
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PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24920 MW;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Embryo;
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01-AUG-1990 (Rel. 15, Last seq
13-SEP-2005 (Rel. 48, Last ann
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HMG1 PIG
ID HMG1 PIG
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Name=HMGB1; Synonyms=HMG1; Sus scrofa (Pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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R PIR, Azaby; File.

R HSSP, P07155; ICKT.

R SMR; P126821 1-83, 92-170.

R GO; GO:0000793; C:condensed chromosome; ISS.

R GO; GO:0008211; F:DNA bending activity; ISS.

DR GO; GO:0006288; P:protein binding; ISS.

DR GO; GO:0006281; P:DNA repair; ISS.

DR GO; GO:0006281; P:DNA repair; ISS.

DR GO; GO:0006281; P:DNA repair; ISS.

DR GO; GO:0006281; P:DNA unwinding; ISS.

DR GO; GO:0006286; P:DNA unwinding; ISS.

DR GO; GO:0006286; P:PNA unwinding; ISS.

DR GO; GO:0006286; P:PNA unwinding; ISS.

DR GO; GO:0006286; P:PNA unwinding; ISS.

DR GO; GO:0006286; P:DNA unwinding; ISS.

DR GO:0006286; P:DNA unwinding; ISS.

DR GO; GO:0006286; P:DNA unwinding; ISS
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 27:6159-6163 (1988).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- SUMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsuda K.-I., Kikuchi M., Mori K., Waga S., Yoshida M.;
"Primary structure of non-histone protein HMG1 revealed by the
nucleotide sequence.";
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PRINTS; PRO0886; HJGHMOBLTY12.
SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS500118; HMG BOX 2; 2.
Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
INIT_MET
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B29C8A32D8D2C933 CRC64;
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                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA]
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10813, Appli
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1018, Ap
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-214-881A-1
US-09-214-881A-3
US-09-214-881A-3
US-09-214-881A-5
US-09-949-016-10813
US-09-949-016-10728
US-09-949-016-10728
US-09-214-881A-2
US-09-214-881A-2
US-09-214-881A-1
US-09-214-881A-189
US-09-736-457-789
US-09-61-325-789
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - protein search, using sw model
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Maximum DB seq length: 200000000
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| Sequence 883, Application US/09538092
| Sequence 883, Application US/09538092
| Patent No. 675334
| GENERAL INFORMATION:
| APPLICANT: Mansfield, Traci A.
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
| FILE REFERENCE: 15566-542
| CURRENT APPLICATION NUMBER: US/09/538,092
| FRIOR APPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SEQ ID NO 883
| LENGTH: 214
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  1667, Ap
1667, Ap
1667, Ap
1667, Ap
1913, Ap
1667, Ap
324, App
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 Sequence 1667,
Sequence 1667,
Sequence 1667,
Sequence 1913,
Sequence 324, P
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US-09-614-124B-1667

US-09-671-325-1667

US-09-658-824-1667

US-10-017-754-1667

US-10-017-754-1913

US-09-651-563-1667

US-09-736-457-324

US-09-611-124B-324

US-09-611-325-324

US-09-689-184-324

US-09-651-563-324

US-09-651-563-324

US-09-651-563-324

US-09-651-563-324

US-09-613-9996-4824

US-09-513-9996-4824
                                                                                                                                                                                                                                                               ALIGNMENTS
  ORGANISM: Homo sapiens
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US-09-214-881A-1

RESULT

10496, A 1667, Ap 1667, Ap

Sequence Sequence Sequence Sequence

US-09-736-457-1667

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  0; Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SOBAJIMA, JUNKO
APPLICANT: SOBAJIMA, JUNKO
APPLICANT: OKAZAKI, TAKANIKO
APPLICANT: TANAKA, MASO
APPLICANT: TANAKA, MASO
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: OSAKAGA, FUMIO
TITLE REFERENCE: 068383.0104
CURRENT PAPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 214
TANDER OF SEQ ID NOS: 2.1
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Pred. No. 1.6e-99;
1; Mismatches 1;
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1; Mismatches
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Patent No. 6822078
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.1%;
Matches 212; Conservative
  213; Conservative
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Patent No. 6822078

GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Osayima Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 13
SEOTIN NO 3
SEOTIN NO 3
SEOTIN NO 3
SEOTIN NO 3
                                                       APPLICANT: OCARL, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 060383.0.04
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.1
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Sequence 1, Application US/09214881A
Patent No. 6822078
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Best Local Similarity 100.
Matches 214; Conservative
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LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Bos taurus
US-09-214-881A-3
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LENGTH: 214
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RESULT 7
US-09-949-016-10728
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; ORGANISM: Human
US-09-949-016-10728
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Patent No. 681239

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WHERE: US/09/949,016

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-03-08

WHIGH APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

WHIGH RELING DATE: 2000-09-08

WHIGH SEQ ID NOS: 207012

SEQ ID NO 10813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Karuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                     98.2%; Score 1128; DB 2; Length 214; llarity 98.1%; Pred. No. 7.5e-99; Conservative 3; Mismatches 1; Indels
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94.8%; Pred. No. 4.2e-92;
tive 3; Mismatches 7; Indels
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Best Local Similarity 94.8
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Rattus rattus US-09-214-881A-5
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Best Local Similarity
Matches 210; Conserv
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ORGANISM: Human
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Sequence 10728, Application US/09949016
| Sequence 10728, Application US/09949016
| Patent No. 6812339
| GENERAL INPORMATION:
| TAPPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: 06/241,755 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR PLILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 10728 |
| LENGTH: 320
123 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 182
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                                                                                                                       SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
IITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
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80.9%; Score 929; DB 2; Length 320;
Best Local Similarity 81.3%; Pred. No. 7.7e-80;
Matches 170; Conservative 19; Mismatches 20; Indels
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Query Match 80.2%; Score 921.5; DB 2; Best Local Similarity 81.4%; Pred. No. 2.3e-79; Matches 171; Conservative 18; Mismatches 20;
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ORGANISM: Sus scrofa
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APPLICANT: Schaima, Junko
APPLICANT: Schaima, Junko
APPLICANT: Usazki, Hiroko
APPLICANT: Usazki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06033.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.1
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                                                                                                                                                               ; LOCATION: (0).7.(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1018
LENGTH: 208
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                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                          ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 208
TYPE: PRT
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61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120
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Sequence 6, Application US/09214881A

Patent No. 6822078

GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 066383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET: 7
SPO TN. NOS: 13
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APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usesugi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nahida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
: TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
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122 IGDVAKKIGEMMNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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                                                                                                                                                              APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Hirokio
APPLICANT: Uesugi, Hirokio
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.0%; Score 827; DB 2; Length 20
74.0%; Pred. No. 2e-70;
ive 23; Mismatches 31; Indels
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STRAED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT FELLING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 879
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181 KKKABPEEEEEEEEDEEEEEEEDEE 206
                                                                                                   Sequence 11, Application US/09214881A Patent No. 6822078
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SEQ ID NO 11
LENGTH: 208
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US-09-914-259-38
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Best Local Similarity
                                                                                 US-09-214-881A-11
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APPLICANT: Sobajima, Junko
APPLICANT: Geusgi, Hiroko
APPLICANT: Usasaki, Takahiro
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Shirdawa, Hitoshi
APPLICANT: Shirdawa, Hitoshi
APPLICANT: Shirdawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISBASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: 1999-06-07
WHORER OF SEQ ID NOS: 13
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                                                                                                                                                                          Query Match 79.7%; Score 915.5; DB 2; Length Best Local Similarity 80.5%; Pred. No. 8.6e-79; Matches 169; Conservative 19; Mismatches 21; Indels
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Patent No. 6822078
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SEQ ID NO 9
LENGTH: 206
                      PatentIn Ver. 2.1
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Matches 165; Conservative
                                                                                      TYPE: PRT ORGANISM: Rattus
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ORGANISM: Gallus gallus
NUMBER OF SEQ ID NOS:
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US-09-214-881A-9
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                               SEQ ID NO 8
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20 VQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYI 79
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usaki, Hiroko
APPLICANT: Usakaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Gaskada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER: OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.1
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70.5%; Score 809.5; DB 2; Length 201;
Best Local Similarity 72.3%; Pred. No. 8.5e-69;
Matches 154; Conservative 21; Mismatches 25; Indels 13
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                                                                                                                                                                                                                                                                                                                                                ; Sequence 10, Application US/09214881A; Patent No. 6822078; GENERAL INFORMATION:
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ORGANISM: Gallus gallus
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EEDDD 878
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US-09-214-881A-10
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Sequence 1, Application US/10147447; Publication No. US20030060410A1; GENERAL INFORMATION:
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Sequence 22, 7
Sequence 74, 7
Sequence 38, 7
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Sequence 2, Al
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Sequence 4,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-17-984-1
US-10-718-945-1
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US-10-918-992-38
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US-10-918-992-10
US-10-918-992-10
US-10-918-992-18
US-10-918-992-18
US-10-14-447-2
US-10-17-984-2
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| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: More David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: NOVEL COMPOSITION OF SURENT PEPLICATION UNMER: US/10/087,192 |
| CURRENT FILING DATE: 2002-03-01 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2001-03-02 |
| PRIOR FILING DATE: 2001-03-02 |
| PRIOR FILING DATE: 2001-03-05 |
| NUMBER OF SEQ ID NOS: 2059 |
| SOFTWARE: FRAESEQ for Windows Version 4.0 |
| SEQ ID NO 1446 |
| LENGTH: 215
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US-10-726-195-5
US-10-300-072-18
US-10-300-072-24
US-10-456-947-10
US-10-456-947-10
US-10-456-947-10
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
US-10-718-495-18
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US-10-456-947-12
US-10-718-495-25
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo Sapien
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Sequence 1, Application US/10300072

Sequence 1, Application No. US2030144201A1

GENERAL INFORMATION:

APPLICANT: Revain J. Tracey

APPLICANT: Hewland Shaw Warren, Jr.

APPLICANT: Mitchell P. Fink

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY

TITLE OF INVENTION: AGENTS

FILE REPERENCE: 3268.1001.005

CURRENT FILING DATE: 2002-11-20

FRIOR FILING DATE: 2002-11-20

FRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2001-05-15

FRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PASTERE (or Windows Version 4.0)

LENGTH. 1.
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100.0%; Pred. No. 3.6e-70;
tive 0; Mismatches 0;
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         APPLICANT: Yang, Huan
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Fink, Mitchell P.
ITILE OF INVENTION: Use of HMG Fragments as
ITILE OF INVENTION: Anti-Inflammatory Agents
FILE REPERENCE: 3268.1001-001
CURRENT APPLICATION NUMBER: US/10/147,447
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
APPLICANT: Tracey, Kevin J. APPLICANT: Yang, Huan
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Best Local Similarity 100.
Matches 215; Conservative
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Matches 215; Conservative
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ORGANISM: Homo sapiens
US-10-147-447-1
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ORGANISM: Homo Sapiens
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61 EDWAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKKGEHPGL 120
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Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Kevin J. Tracey

TITLE OF INVENTION: HMIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: AMTI-INFLAMMATORY AGENTS

FILE REFERENCE: 3268.1001-007

CURRENT APPLICATION NUMBER: US/10/456,947

CURRENT FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: 10/147,447
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100.0%; Pred. No. 3.6e-70;
iive 0; Mismatches 0;
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Publication No. US2004005316A1;
GENERAL INPORMATION:
APPLICANT: Huan Yang
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS;
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS;
TITLE OF INVENTION: USE OF HMG FRAGMENTS;
FILE REFERENCE: 3268.1001-006
CURRENT FILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 10/147,447
FRIOR FILING DATE: 2002-05-15
FRIOR FILING DATE: 2002-05-15
FRIOR FILING DATE: 2001-05-15
FRIOR FILING DATE: 201-05-15
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Best Local Similarity 100.
Matches 215; Conservative
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Query Match 100.0%; Score 1149; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
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; Pred. No. 3.6e-70;
0; Mismatches 0;
                                                    Sequence 1, Application US/10717984

Publication No. US20040156851A1

GENERAL INPORMATION:

APPLICATION Walter

TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES

FILE REFERENCE: 3258.1008-001

CURRENT APPLICATION NUMBER: US/10/717,984

CURRENT FILING DATE: 2003-11-20

PRIOR PILING DATE: 2002-11-20

PRIOR PILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE PASESEQ for Windows Version 4.0

SEQ ID NO 1
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Best Local Similarity 100.0
Matches 215; Conservative
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TYPE: PRT
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                                                                                                                                                                                                                                                        0; Indels
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Publication No. US20040141948A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa L.
TITLE OF INVENTION: USE OF HAGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR PILING DATE: 2003-11-12
NUMBER: OF SEQ ID NOS: 58
SOFTWARE: FRACERO for Windows Version 4.0
                                                                                                                                                                                                                                                      0; Mismatches
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                      Matches 215; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-718-495-1
                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                     LENGTH: 215
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US-10-718-495-1
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; Sequence 63, Application US/10868577A
; Publication No. US20050032697A1
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.;
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/33359A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR APPLICATION NUMBER: 2003-08-12
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PATENTIN VERSION 3.2
; SEQ ID NO 63
; LENGTH: 215 ठे Length 215;

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Query Match
Best Local Similarity 100.0
Matches 215; Conservative
 ; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-74
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PUblication No. US20050043235A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al.

TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY

FILE REPERENCE: 29967/39117A

CURRENT APPLICATION NUMBER: US 60/478,114

PRIOR FILING DATE: 2003-06-12

PRIOR APPLICATION NUMBER: US 60/478,114

PRIOR FILING DATE: 2003-06-12

PRIOR APPLICATION NUMBER: US 60/478,390

PRIOR APPLICATION NUMBER: 203-06-12

PRIOR SEQ ID NOS: 25

SOPTWARE: PatentIn version 3.2
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100.0%; Pred. No. 3.6e-70;
ive 0; Mismatches 0; Indels
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APPLICANT: Qin, Shixin
APPLICANT: O'Keefe, Theresa
APPLICANT: Obar, Robert
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT PELLING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: 60/502,568
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-938-992-74
; Sequence 74, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
APPLICANT: Newman, Walter
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Best Local Similarity 100.(
Matches 215; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-549-22
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US-10-868-549-22
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Publication No. US20050152903A1

GENERAL INFORMATION:

APPLICANT: Newman, Walter

APPLICANT: Oin, Shixin

APPLICANT: O'Keefe, Theresa

APPLICANT: Obar, Robert

TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1

FILE REFERENCE: 3258.1033-001

CURRENT APPLICATION NUMBER: US/10/938,992

CURRENT FILING DATE: 2004-09-10

PRIOR FILING DATE: 2003-09-11
                                                    Indels
; Score 1149; DB 5;
; Pred. No. 3.6e-70;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 215
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US-09-214-881A-1
; Sequence 1, Application US/09214881A
100.0%;
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Best Local Similarity 100.0%; Pred. No. 7.8e-70; Matches 214; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8e-70;
Matches 214; Conservative 0; Mismatches (
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JOSAKI, Shoichi
JOSAKI, Shoichi
SOBAJIMA, Junko
HELICANT: Gebugi, Hiroko
HAPLICANT: Deazaki, Takahiro
HAPLICANT: Tanaka, Masao
HAPLICANT: Tanaka, Masao
HAPLICANT: Ankao, Kazuwa
HAPLICANT: Shirakawa, Hitoshi
HAPLICANT: Shirakawa, Hitoshi
HIERERERERENCE: O68434, O104
HILE REFERENCE: 06833.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver 7
LENGTH.
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APPLICANT: Sobajima, Junko
APPLICANT: Wesuaj, Hiroko
APPLICANT: Osazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TILE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/10/726,195
CURRENT FILING DATE: 2003-12-02
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEC ID NOS: 13
SOFTAME: Patentin Ver. 2.1
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100.0%; Pred. No. 7.8e-70;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.6
Best Local Similarity 100.
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1
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LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
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99.6%; Score 1144; DB 5; Length 214;

Query Match

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APPLICANT: Qin, Shixin
APPLICANT: O'Neefe, Theresa
APPLICANT: O'Neefe, Theresa
APPLICANT: O'Neefe, Theresa
APPLICANT: O'Neefe, Theresa
TITLE OF INVENTION: Monoclonal Antibodies Against HWGB1
TITLE OF INVENTION: MONOCLONAL
CURRENT APPLICATION NUMBER: 00/10/938,992
CURRENT PILING DATE: 2004-09-10
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SSOTUANG DATE: 2003-09-11
SSOTUANG: ZEBLESQ for Windows Version 4.0
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; Sequence 2, Application US/10147447
; Publication No. US2030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
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121 SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Fink, Mitchell P.
TITLE OF INVENTION: Use of EMG Fragments as
TITLE OF INVENTION: Use of EMG Fragments
FILE REPERENCE: 3268.1001-001
CURRENT APPLICATION NUMBER: US/10/147,447
CURRENT APPLICATION NUMBER: 06/291,034
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 215
TYPE: PRI
ORGANISM: MUS MUSCUlus
US-10-147-447-2
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Job time : 204.391 secs
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Best Local Similarity 99.1
Matches 213; Conservative
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US-11-186-422-11
Sequence 11, Application US/11186422
; Publication No. US20060057679A1
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GenCore version 5.1.7
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US-11-172-740-1566
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US-10-10-192-14
US-10-19-150-14
US-10-19-150-14
US-11-186-422-14
US-11-186-422-13
US-11-087-099-8879
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Sequence 21031, A
Sequence 21031, A
Sequence 21033, A
Sequence 21033, A
Sequence 9681, Ap
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US-11-096-568A-32733
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US-11-096-568A-26884
US-11-096-568A-26884
US-11-096-568A-3510
US-11-096-568A-3510
US-11-096-568A-31033
US-11-096-568A-31033
US-11-096-568A-3103
US-11-096-568A-3103
US-11-096-568A-3103
US-11-096-568A-3103
US-11-096-568A-3103
US-11-096-568A-3103
US-11-096-568A-3681
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                                                                                                                                                                                                                                                                                                                                                                                              US-11-087-099-869
US-11-087-099-9518
US-11-087-099-8838
US-11-124-368A-308
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US-10-821-234-1443
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us-10-717-984-1.rapbn

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192
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Sequence 12, Application US/11186422
Fublication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Ucciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3288.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT PILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FRASESO for Windows Version 4.0
             APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Oin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3288.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
NUMBER OF EGO ID NOS: 34
SOFTWARE: FASESQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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LENGTH: 215
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LENGTH: 215
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Squence 192, Application US/11169041

Squence 192, Application US/11169041

Squence 192, Application US. US2006019284A1

GENERAL INFORMATION:

JENUTICAL OF UNVENTION:

TITLE OF INVENTION:

CELLS

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT APPLICATION NUMBER: 60/584,405

PRIOR PILLING DATE: 2004-06-20

NUMBER OF SEQ ID NOS: 527

SOFTWARE: Patentin version 3.2

LENGTH: 879
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Sequence 1234, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TITLE OF INVENTION: Wethods for Diagnosis and Treatment of Preeclampsia

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt SEQ_genes Version 1.0

SEQ ID NO 1234
61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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71.8%; Score 824.5; DB 7; Length
Best Local Similarity 85.4%; Pred. No. 6e-53;
Matches 158; Conservative 9; Mismatches 17; Indels
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TYPE: PRT ORGANISM: Daucus carota
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                                                                                                                                                                                                          Query Match 59.3%; Score 681; DB 6; Length 169; Best Local Similarity 75.1%; Pred. No. 3.2e-43; Matches 127; Conservative 13; Mismatches 29; Indels
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APPLICANT: Kevin J. Tracey
APPLICANT: Haichao Wang
TITLE OF INVENTION: ANTACONISTS OF HMG1 FOR TREATING
TITLE OF INVENTION: 10PLAMMATORY CONDITIONS
FILE REPERENCE: 3268.1000-011
CURRENT APPLICATION NUMBER: US/10/719,150
                                                                                      NAME/KEY: misc_feature; LOCATION: (1)...(169); OTHER INFORMATION: Xaa = any amino acid or nothing US-10-821-234-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/11186422
Publication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
ITILE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT PELING DATE: 2005-07-20
CURRENT PILING DATE: 2005-07-20
PRIOR FILING DATE: 2004-07-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 69
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                                           ORGANISM: Homo sapiens
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US-10-719-150-6
LENGTH: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 89.9, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION: US20060041961A1
GENERAL INFORMATION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53450) B EP;
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
SEQ ID NOS: 12464
SEQ ID NOS: 12464
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 287; DB 6; L
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 25.0%; Score 287; DB 7; I
1 Similarity 100.0%; Pred. No. 5.7e-15;
54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/11186422;
Publication No. US20060057679A1;
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
TILE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT APPLICATION NUMBER: 06/589,678
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 54
PRIOR APPLICATION NUMBER: US/10/300,068
PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20
PRIOR PLING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 10/210,747
PRIOR PRIOR DATE: 2000-02-14
PRIOR PRIOR DATE: 2000-02-14
PRIOR PRIOR DATE: 1990-02-14
PRIOR PLING DATE: 1999-02-11
PRIOR PLING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-10-719-150-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 54; Conserv
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OTHER INFORMATION: Utility: Useful for making plants with increased biomass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KADKARYEREMKTYIPPKG-----ETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 -GLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- 106
                                                                                                                                                                                                                                                     2 KGGKSKAKSDNKLAVKKRGCETKKSKKSVKDPNKPKRPPSAFFVFMEDFRKTYKEKHPNN
                                                                                                                                                                                                                                                                                                                                                                  120 LSIGDVAKKLGEMMNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KADAKAADNRLKR----KGAGAGRKQSKKAAKDPNKPKRPPSAFFVFMSEFREQYKKEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Gaps
                                                                                                                                                                   10;
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UG-11-087-099-3510
; Sequence 3510, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21 (53450)B BP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3510
                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(543450) B EP
CURRENT APPLICATION UNMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AEKSKKKKEEEEDEEDEEDEEBEEBDEDEEBDDDDE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 -RKLEGKNPSEEEKSDK--SKSEVNDEDEDEEEDQDDE 141
                                                                                                         Query Match

23.8%; Score 273; DB 7;
Best Local Similarity 37.3%; Pred. No. 1.7e-13;
Matches 56; Conservative 31; Mismatches 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.3%; Score 268; DB 7; Best Local Similarity 39.2%; Pred. No. 3.8e-13; Matches 62; Conservative 23; Mismatches 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 ESDKSRSEVNDDEEDEDGSAEDDDDDDDD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                             180 KSKKKKEEEEDEEDEEDEEEEDEEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3073, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Canavalia gladiata
US-11-087-099-3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Vicia faba
                                                      US-11-172-740-1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-087-099-3073
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  LOCATION:
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APPLICANT: MASCILA, Peter
APPLICANT: MASCILA, Peter
APPLICANT: MASCILA, Peter
APPLICANT: BROWEN, Vacchedatav
TITLE OF INVENTION: NUCLECTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE REFERENCE: 2750-1602PUS2
CURRENT PAPLICATION NUMBER: 08/11/172,740
CURRENT FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
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LOCATION:
OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leave
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Utility: Useful for making ornamental plants with modified
                                                                                                            8
                                                                                                                                                                                                  279 KKTKKEKDPLKPKHPVSAFFLFMNERRADLVAEKK--NVLEVGKITGEEWKNMTEKEKAP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKPYEEKYQAEKEAYLKIVGAEKRENEAMKILEEEQKQRTAMELLEQYMQFKEETENDKK 278
                                                                                                                                                                                                                                                                                                                                                                                   ---KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKOP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 YEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSK------KKKEEEEDEED 193
                                                                                                                                                             1 MGKGDPKK--PRGKMSS--YAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKE
                                                                                                      51;
                                                         Length 502;
                                                                                                            86; Indels
                                             DB 7;
                                                                                                                                                                                                                                                                         KGKFEDMAKADKARY---------EREMK---
                                                   24.2%; Score 278.5; DB 7
31.8%; Pred. No. 2.5e-13;
iive 39; Mismatches 86
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OTHER INFORMATION: Public GI no. 1052956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : || :: :: | : KTKEEROKKOKGEKKIVD 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEDEEEEDEEDEDEED 211
                                                   Query Match 24.29
Best Local Similarity 31.89
Matches 82, Conservative
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NAME/KEY: misc_feature
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ORGANISM: Glycine max
US-11-087-099-8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-11-172-740-1569
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62 KSVAAVGKAGGDAWKKLSEAEKAPYQAKAEKRKAEYQKNMDAYNRKQAGDA-----BED 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 IKGEHP-GLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 KADKARYEREMKTYIPPKG----ETKKKFKDPNAPKRPPSAFFLFCSEVRPKIKGEHP-G 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAE 179
                                         KGEHP-GLSIGDVAKKLGEMMNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AKSKG----AAKADTKLAVKSKGAEKPAAKGKKGKAGKDPNKPKRAPSAFFVFMGEFREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 160;
                                                                                           | :||  |:  ||  ||  |:  |:  ||  ||  |:  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  || 
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                                                                                                                                                                                                                                                    173 KGVVKAEKSKKKKEEBEDEEDEEDEEDEEDEDEBEBDDDD 214
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Publication No. US20060041961A1
GRERAL INFORMATION:
GRERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B.FP
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.3%; Score 267.5; DB 7
Best Local Similarity 39.6%; Pred. No. 4.8e-13;
Matches 65; Conservative 24; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1105, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Nicotiana tabacum
US-11-087-099-4976
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-087-099-1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-087-099-1105
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| Sequence 1571, Application WS/11172740
| Publication No. US20060057724A1
| GENERAL INFORMATION:
| APPLICANT: MASCIA, Peter
| APPLICANT: ALEXANDROY, Nickolai
| APPLICANT: ALEXANDROY, Nickolai
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
| TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
| TITLE OF INVENTION: NUMBER: 0S/0583,621
| FRIOR REPLICATION NUMBER: 60/583,621
| PRIOR PELLING DATE: 2004-06-30
| PRIOR PILING DATE: 2004-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: _ _
OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: Utility: Useful for making ornamental plants with modified flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JTHER INFORMATION: Utility: Useful for making ornamental plants with modified leavee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                           58 GKFEDMAKADKARYEREMKTYI PPKGETK----KKPKDPNAPKRPPSAFFLFCSEYRPKI 113
                                                                                                                        58 GKFEDMAKADKARYEREMKTYIPPKGETK----KKFKDPNAPKRPPSAFFLFCSEYRPKI 113
                                                                                                                                                                                                                                                                                 114 KGEHP-GLSIGDVAKKLGEMWNYTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
                                                                                                                                                                                                  GKSKGESKKAETKLAVNKKGAAATKGGKKPAKGKEPKDPNKPKRPPSAFFVFMADFREQY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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35.8%; Pred. No. 4.4e-13;
tive 29; Mismatches 54; Indels
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-----NKKLEGKDDEEGSDKSKSEVNDEDEDEEDEEDEEDDD 149
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LOCATION: (1)._(149)
OTHER INFORMATION: Public GI no. 729737
Best Local Similarity 35.8
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Conservative
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NAME/KEY: misc_feature
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LOCATION:
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Search completed: April 6, 2006, 10:33:30 Job time : 26.875 secs

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6, 2006, 10:33:08 ; Search time 189 Seconds (without alignments) 499.822 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 MGKGDPKKPRGKMSSYAFFV......DEEEEEDEEDEDEDDDE 215 2443163 segs, 439378781 residues OLIGO Gapop 60.0 , Gapext 60.0 US-10-717-984-1 Perfect score: Scoring table: Sequence: Searched: Title:

2442881 Total number of hits satisfying chosen parameters:

Word size :

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Listing first 45 summaries

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_21:* 1: geneseqp198 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	199	359	789	788	577	191	918	177	922	208	110	343	248	326	385	304	545	147	980	984	732	728	280
BCr:	Abu07499	Aae35859	Add40789	Add40788	Abm85677	Ado60491	Ado25918	Ado71477	Adr45922	Abm81508	Adw81011	Adx69343	Ady14248	Ady85326	Ady85085	Adz80804	Add47645	Ade60447	Ade57980	Ade57984	Ade60732	Ade60728	Ads17580
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	ABU07499	AAE35859	ADD40789	ADD40788	ABM8567	ADO6049	AD025918	AD07147	ADR45922	ABM81508	ADW8101	ADX69343	ADY14248	ADY85326	ADY85085	ADZ80804	ADD47645	ADE6044	ADE57980	ADE57984	ADE60732	ADE60728	ADS17580
90	. 9	9		7	7	~	8		8	. 8	6	٦ 6	6	٦ 6	6	6	7	7	7	7	_	7	. 8
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Length	21	21	21	215	21	21	21	21	21	21	21	21	21	21	21	21	21,	21,	214	21	21,	21	21
	. 0	0	0.	0.	0.	0.	100.0	0.	0.	100.0	0.	100.0	100.0	0.	100.0	0.	99.5	99.5	99.5	9.5	9.5	9.5	.5
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100	100.0	100.0	2	100.0	2	5	100.0	5	100.0	9	9	99	99	6	6	66
re	215	15	215	15	215	15	215	215	15	15	15	12	215	15	15	15	214	214	214	214	214	14	214
Score	. 7	N	N	7	7	7	7	N	~	8	7	~	7	N	7	7	N	N	N	7	7	~	0
Result No.	-	7	m	4	S	9	7	8	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Abb57220 Mouse isc Abc57220 Mouse and		Adv85327 Mouse and Adv85376 Mouse pro Adv85016 Human HMG	Rat	Ade5/982 kat Prote Ade60726 Rat Prote Ade60445 Rat Prote		Aea90125 Human hig Abm81641 Tumour-ae Ady85029 Rat and m
ABP64829 ABB57220 AAE35860	AD025919 AD071478	ADY85327 ABM85676 ADY85016	ADE60730 ADE57978	ADE57982 ADE60726 ADE60445	AAY73828 ADA55380	AEA90125 ABM81641 ADY85029
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ALIGNMENTS

RESULT 1 ABU07499

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer monitoring. Protein differentially regulated in prostate cancer #102. ABU07499 standard; protein; 215 AA. 08-APR-2002; 2002WO-US010824. 06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P. (first entry) WO200281638-A2. 28-JAN-2003 Homo sapiens 17-0CT-2002. ABU07499;

(ORIG-) ORIGENE TECHNOLOGIES INC. WPI; 2003-058520/05. N-PSDB; ABX10404 Jay G; Sun Z,

Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 413-414; 416pp; English.

The invention describes genes (1) which are differentially regulated in prostate cancer. (1) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of trarget genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (1) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.

Ady85051 Human HMG

9 ADY85051

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Trerestably, the explication of a creat that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially regulated cancer cells, which involves contacting a polypeptide differentially regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulates the biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as markers, as drug targets, and for determing, clasquosing, staging, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide encoded by (I) can be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and thus concerned to respect the definition of prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways concerned by prostate cancer permits the definition of the pathways which are useful in diagnostic, therapeutic, and clinically concerned applications. This is the amino acid sequence of a protein differentially concerned and concerned and disease pathways and the delineations differentially
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    Preferably, the expression levels of at least 10 genes are determined
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Matches 215; Conserv
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Key Binding-site

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The invention relates to high mobility group (HMG) protein comprising DNA binding motifes termed HMG A box and HMG B box. HMG A box or a non-auturally occurring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's disease, peritonitis, employeema, HIV infection, candidissis, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocardiis, myocardial ischaemia, meningitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's asyndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMGI (also termed as HMGBI)
                                                                                                                                                                                                                                                                                                                                      New isolated polypeptide having a vertebrate HMG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.
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 binding motif (HMG1 A box)"
                                 binding motif (HMG1 B box)"
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                 89. .162
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UNIV PITTSBURGH.
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Best Local Similarity 100.
Matches 215; Conservative
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                   Binding-site
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(UYPI-)
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disease;

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This invention describes a novel method comprising using high mobility group B proteins (HMGB) as target molecules for development or group B proteins (HMGB) as target molecules for development or compositions (compositions of compositions) as contraceptives. The products of the invention care used in kit for characterising the status of the endometrium, compositions to presence of pregnancy or irregularities in the menstrual cycle. The proteins used in the invention can be HMGB, 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor for dawneed glycation end products). The products of the invention have gynaecological, contraceptive and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products). In products of the invention have gynaecological, contraceptive and cytostatic activity. HMGB is part of a nuclear transcription factor complex and, extracellularly, a ligand for involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometrions or polyps, hyperplasia or carcinoma of the endometrium, particularly for detecting pregnancy or menstrual disorders. This sequence represents the human HMGB1 protein used in the method of
                                                        high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease, contraceptive; endometrium; pregnancy; menstrual cycle irregularity; RAGE; receptor for advanced glycation end; gynaecological; cytostatic; nuclear transcription factor complex; tumour metastasis; endometriosis; polyps; hyperplasia; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developing treatment and diagnosis of endometrial disorders, using mobility group B proteins, or related nucleic acid or interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 43pp; German.
                                                                                                                                                                                                                                                                                                                                                       19-DEC-2002; 2002WO-EP014579
                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001DE-01062556
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALCE-) ALCEDO BIOTECH GMBH.
                           Human HMGB1 protein #2.
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                                                                                                                                                                                                                Homo sapiens
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ö Gaps ö Length 215; 100.0%; Score 215; DB 7; Length 2: 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 215; Conservative 8

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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL

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group B proteins (HMGB) as target method comprehensing institution of compositions (for treatment, prevention or diagnosis of preparation of compositions (for treatment, prevention or diagnosis of endometrial diseases, or as contraceptives. The products of the invention are used in kit for characterising the straus of the endometrium, especially for presence of pregnancy or irregularities in the menstrual order. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor for advanced glycation end products). The products of the invention have synaecological, contraceptive and cytostatic activity. HMGB is part of nuclear transcription factor complex and, extracellularly, a ligand for the surface RAGE (receptor for advanced glycation end products) which is involved in tumour metastasis. The products of the invention are used to develop treatments, preventions or diagnoses of endometrial disease, particularly endometricials or polyps, hyperplasia or carcinoma of the endometrium, also contraceptives and methods for assessing status of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endometrium, particularly for detecting pregnancy or menstrual disorders. This sequence represents the human HMGB1 protein used in the method of
                                                                                                                                                                                 endometrial disease;
                                                                                                                                                                                                  contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
nuclear transcription factor complex; tumour metastasis; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Developing treatment and diagnosis of endometrial disorders, using high mobility group B proteins, or related nucleic acid or interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method comprising using high mobility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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                                                                                                                                                                                 protein; HMGB1; HMGB2; HMGB3;
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              ADD40788 standard; protein; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 43pp; German.
                                                                                                                                                                                                                                                                  carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2002; 2002WO-EP014579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2001; 2001DE-01062556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALCE-) ALCEDO BIOTECH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 215; Conservative
                                                                                                                                                                               mobility group B
                                                                                                                                                                                                                                                                  polyps; hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          partners, as targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-505462/47.
N-PSDB; ADD40787.
                                                                                                                                      Human HMGB1 protein.
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                                                                                                                                                                                                                                                                                                                                               WO2003051383-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bullerdiek J;
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2003.
                                                         ADD40788;
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ADO60491 standard; protein; 215
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                                                                                                                                                               15-JUL-2004 (first entry)
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Les 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 215 AA;
                                                                                                                                                                                                                                                                                                     JP2004107260-A.
                                                                                                                                                                                                                                                                             Homo sapiens
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  121
                           181
                                                                                                                                      ADO60491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel DNA and protein sequences which ser associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (ix) for diagnosing carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as markers of carcinoma including lymphoma. The present sequence is one such CAP. Note: This patent is an equivalent to basic patent US2002182586AI, for which no sequence data was published
SIGDVAKKLGEMMNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
              SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
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                                                               SKKKKEEEEDEEDEEDEEDEEDEEDEEDEBDDDB 215
                                                                                                                                                                                                                                       Cytostatic; carcinoma; lymphoma; cancer; human.
                                                 SKKKKEREEDEEDEEDEEDEEDEEDEEDDDE
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                                                                                                                                      Ą.
                                                                                                                                     ABM85677 standard; protein; 215
                                                                                                                                                                                                             Human protein sequence hCP43793.
                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                                        28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
1es 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-328604/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 215 AA;
                                                                                                                                                                                                                                                                                      WO2003073826-A2
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                     18-NOV-2004
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This invention relates to a novel vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytosis by microglia, which comprises a high mobility group protein 1 (HMG1), its partial peptide, or its salt. The invention may be useful for the production of compounds with a nootropic or neuroprotective activity acting as promoters of inhibition of amyloid beta 42 aggregation or promoters of amyloid beta 42 phagocytosis by microglia. The invention may also be useful for the production of a vaccine. The invention is useful for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy or preventing brain amyloidosis such as Alzheimer's disease. The present sequence is that of the protein encoded by the human high mobility group protein 1 (HMG1) gene which may be used during the creation of the novel
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vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis; microglia; high mobility group protetin 1; HMG1; nootropic; neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy; brain amyloidosis; Alzheimer's disease; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine for promoting amyloid beta 42 aggregation inhibitory effect and/or amyloid beta 42 phagocytosis, useful for prophylaxis and/or treatment of Alzheimer's disease or Down's syndrome, comprises high
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human high mobility group protein 1 (HMG1) protein SeqID2.
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; Pred. No. 8.2e-195;
0; Mismatches 0;
                                                                                                                                                                    SKKKKEEEEDEEDEEDEEBEEEBEEDEEDEEBDDDE 215
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Thu: Apr

SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

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The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) that can be used to stimulate cytokine activity and increase immune response to assist in treating disease.
                    SIGDVAKKLGEMMNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKDDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
SIGDVAKKLGEMWINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                    cytostatic; gene therapy; vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity.
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                                                                                                   SKKKKEEEEDEEDEEDEEDEDEDEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 1; 68pp; English.
                                                                                                                                                                                                                                                                                                                             Human high mobility group box 1 (HMG1)
                                                                                                                                                                                                              AD025918 standard; protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-2003; 2003WO-US036975.
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                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to one. B proinflammatory cytokine from a cell treated with HMGB, a method for composition comprising an HMGB protein or an antibody that binds to the fectual whether a compound inhibits inflammation, a pharmaceutical determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMP biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the plypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                                 Human; high mobility group box 1, HMGB1; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; reportionitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Bahcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, mycoradial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence
                                                                                                                                                                                                                                                                                                                                                         Human high mobility group box 1 (HMGB1) protein #1
                                                                 215
                                                                                           181 SKKKKEEEEDEEDEEDEEEEEDEEDEEDEEDDDE 215
                                                               181 SKKKKEEEEDEEDEEDEEEEDEEDEEEDDDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                        ADO71477 standard; protein; 215
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20-NOV-2002; 2002US-0427846P.
                                                                                                                                                                                                                                                                                                               26-AUG-2004 (first entry)
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Gaps ö

0; Indels

0; Mismatches

Matches 215; Conservative

Similarity

Local

Query Match

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MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 1 MGKGDPKKPRGKMSSYAPFVQTCREEHKKKHPDASVNPSBFSKKCSERWKTMSAKEKGKP

EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAPFLFCSEYRPKIKGEHPGL 120 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

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degeneration, arthritis, endometriosis, histiocytosis, psoriasis, rosacca, eruptive or cavernous haemangioma, tumours (especially melanoma, Raposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis, angina pectoris, ischaemia, infarction, infertility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, leather skin', skin cancers and ageing (including where associated with sunburn) and cardiac infarct, including cosmetic treatment, especially as a sun-protection composition. Compounds identified as modulators of the specified processes can also be used therapeutically. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGDVAKKLGEMWINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human, overexpression, cancer; tumour; diagnosis, cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target (TAT) polypeptide PRO71096, SEQ:3888.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
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    (proliferative) diabetic retinopathy, diabetic nephropathy, macular
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                    100.0%; Score 215, DB 8; Length 215; 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0; Indels (
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Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; cytostatic.
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                                                                                                                                                                                                                                                                            Sequence 215 AA;
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                                                                                                                                                                                                                                                                                                                        Query Match
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human.
                                                                                                                                                                                                                                                                         EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of nucleic acids encoding basic DNA-binding proteins, and their translation or transcription products, for treating diseases associated with e.g. angiogenesis, neovascularization or wound healing, also for
                                                                                                                                                                                  1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                             MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antidiabetic; ophthalmological; nephropathic; antiarthritic; antiinflammatory; cytostatic; gynaecological; antipsoriatic; dermatological; antiviral; vasotropic; antiarteriosclerotic; cardiant; vulnerary; antiulcer; high mobility group protein;
                                                                                           Length 215;
                                                                                                                                   Indels
represents a human HMGB1 polypeptide of the invention.
                                                                                    ; Score 215; DB 8; I
; Pred. No. 8.2e-195;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKKKKEEEEDEEDEEDEEEEEDEDEEEDEDDDE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human high mobility group protein HMGB1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR45922 standard; protein; 215
                                                                                         100.0%;
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2003DE-01010160.
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                                                                                  Query Match
Best Local Similarity 100.
Matches 215; Conservative
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                                            Sequence 215 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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07-MAR-2003;
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RESULT

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objypeptides, and their related nucleic associated antigence of carget. That it conversoresed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide properties at least 80% identical to the TAT nucleic acids and polypeptide and antibody specific for a TAT polypeptide; fusion proteins comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancers such as breast cancer, colorectal cancer, lung cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide.
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                                                                                     The invention relates to human tumour associated antigenic target (TAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 215; DB 8; L 100.0%; Pred. No. 8.2e-195;
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                                         Claim 12; SEQ ID NO 3888; 7273pp; English.
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Best Local Similarity 100.
Matches 215; Conservative
  prostate cancer or tumor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 215 AA;
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14-JUN-2004; 2004WO-US019197.

WO2005011722-A2

10-FEB-2005

Homo sapiens

amphoterin

9

Gaps

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The present invention relates to new vascular endothelial growth factor (VEGF) proteins useful for skin healing of a skin graft onto underlying tissue. The method involves contacting a skin graft/flap or underlying tissue with an agent chosen from vascular endothelial growth factor C (VEGF-C) polymucleotides, vEGF-C polypeptides, VEGF-D polymucleotides, or amount effective to reduce edema or increase perfusion at skin graft or flap. The composition comprises a gene therapy vector that encodes VEGF-C polymotleotide. The VEGF-C polypeptide or comprises the formula X-B-Z or Z-B-X, where X binds VEGF receptor-3 (VEGFR-3) and comprises a VEGFR-3 ligand amino acid sequence chosen from a prepro-VEGF-C sequence, and fragments that binds VEGF-3, where Z comprises a heparin-binding amino acid sequence, and B comprises a covalent attachment linking X to Z. The VEGF-C polymucleotides, VEGF-C polymucleotides, and VEGF-D polympeptides, VEGF-D polymucleotides, and VEGF-D polympeptides, VEGF-D polymucleotides, and VEGF-D polympeptides, VEGF-D polymucleotides, and VEGF-D polympeptides, VEGF-C polymotleotides, vEGF-C polymotleotides (VEGF-C polymotleotides, VEGF-C polymotleotides, vEGF-C polymotleotides (VEGF-C polymotleotides (VEGF-C polymotleotides), vEGF-D polympeptides, vEGF-D polymotleotides, and VEGF-D polympeptides, vEGF-C polymotleotides, vEGF-C polymotleotides, vEGF-C polymotleotides, vEGF-C polymotleotides, vEGF-C polymotleotides, vEGF-C polymotleotides (VEGF-C polymotleotides), vEGF-D polymotleotides, vEGF-D polymotleotides, vEGF-C polymotleotides (VEGF-C polymotleotides), vEGF-D polymotleotides, vEGF-D polymotleotide
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                                                                                                                                                                                                                                                                               Improving healing of akin graft or akin flap to underlying tissue useful in mastopexy, cosmetic surgery, abdominoplasty, involves using composition of vascular endothelial growth factor-C or D polynucleotides and/or polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                                                                                                                                                        Asko-Seljavaara S;
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                                                                                                                                                        Tammela T,
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100.0%; Pred. No. 8.2e-195;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; SEQ ID NO 22; 119pp; English.
                                                                                                                                                        Karkkainen M,
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                                                                         (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
12-JUN-2003; 2003US-0478114P.
12-JUN-2003; 2003US-0478390P.
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Matches 215; Conservative
                                                                                                                                                     Saaristo A,
a S, He Y;
                                                                                                                                                                                                                                 WPI; 2005-142834/15.
                                                                                                                                                                             Yla-Herttuala S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 215 AA;
                                                                                                                                                  Alitalo K,
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The invention relates to heparin-binding vascular endothelial growth factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The heparin binding VEGFR-3 proteins are used for stimulating growth of mammalian endothelial are used for stimulating the growth of mammalian endothelial cells, amammal, and for modulating the growth of mammalian endothelial cells. The polypeptide may also be used for promoting recruitment, proliferation, differentiation, migration or neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral sclerosis (ALS), dementia, or cerebral palsy. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDMAKADKARYEREMKTYIPPKGETKKKKFKDPNAPKRPPSAFFLFCSBYRPKIKGEHPGL 120
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                                                                     amphoterin; Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian; Anticonvulsant; VEGF-3 receptor; Angiogenesis stimulator; Gene Therapy; vascular endothelial growth factor receptor 3; VEGFR-3; angiogenesis disorder; neurodegenerative disorder; Alzheimers disease; perkinsons disease; motor neuron disease; dementia; paralysis; VEGF-C; neurological disease; Huntingtons chorea; vascular endothelial growth factor receptor 3; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-2003; 2003US-0478390P. 23-SEP-2003; 2003US-00669176.
                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-2003; 2003US-0478114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tammela T;
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(first entry
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Les 215; Conservative
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                                                                                                                                                                                                                                          Homo sapiens
05-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosining and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
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                                                                                                                            Antiinflammatory, Immune disorder; Dermatological; Immunosuppressive; Antiirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis.
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Best Local Similarity 100.0%; Score 215; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0: Tradela '
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ADY14248 standard; protein; 215 AA.
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                                                               (first entry)
                                                                                              polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-182330/19
                                                                                                                                                                                                                                                                                                                                                                                                                        Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 215 AA;
                                                                                                                                                                                                                                                          WO2005016962-A2
                                                                                                                                                                                                                             Homo sapiens
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                                                              05-MAY-2005
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                               ADY14248;
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9

ADY85326 standard; protein; 215 AA.

(first entry)

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Human high mobility group box protein HMGB1.
    02-JUN-2005
                  Homo sapiens
                                24-MAR-2005
 ADY85326;
                       Region
                         Region
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The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-human antigen, non-agine and individual, by the transplantation of an organ into the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of altividual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering HMGB A box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of the vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate HMGB A box, or an immunosuppressive fragment or comprises administering a wertebrate HMGB A box, or an immunosuppressive fragment or non-naturally-occurring HMGB A box, or an immunosuppressive an immunosuppressive an immunosuppressive and a successive an immunosuppressive and a successive and an immunosuppressive and a successive and an immunosuppressive and a successive and an immunosuppressive and and a successive and an immunosuppressive and and an immunosuppressive and and an immunosuppressive and an imm Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment. High mobility group box; HWGB1; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcertative colitis; antiaflammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiathmatic; remarked arthritis; antirheumatic; antiathritis; antiathreumatic; antiathritis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer. B fragment of these, and a vertebrate or non-naturally-occurring HMGB E box. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, psoriasis or systemic lupus erythematosus (all claimed). The present sequence is that of the human HMGBI protein, which can be used as the HMGB polypeptide in methods of the invention. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES Claim 6; SEQ ID NO 1; 57pp; English. Location/Qualifiers 32. .85 /label= A_box /label= B_box 10-SEP-2004; 2004WO-US029540. 10-SEP-2003; 2003US-0502349P (GEHO) GEN HOSPITAL CORP .161 Warren HS, Tracey KJ WPI; 2005-233421/24. WO2005025604-A2

Disclosure; SEQ ID NO 2; 123pp; English. ŭ Obar Okeefe T, WPI; 2005-233483/24. Qin S, Newman W, as the

Sequence 215 AA;

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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                                                                                            SIGDVAKKLGEMWINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HWGB) polypeptide, to acthods of detecting and/or identifying an agent that binds to an HWGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibite release of a proinflammatory cytokine from a cell treated with HMGB protein, useful for treating, e.g. sepsis.
                                                                                        1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTWSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High mobility group box; HMGB1; monoclonal antibody; antibody therapy, sepsis, antibacterial immunosuppressive; graff rejection; arthritis; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress promice obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory; bowel disease; astrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
                                                                    1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                    Gaps
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 Length 215;
                                  Indels
100.0%; Score 215; DB 9; I. 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0;
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 Query Match 100.
Best Local Similarity 100.
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HMGB1 A box.
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detecting an HMGB polypeptide in a sample. The antibody (or antigen-
binding fragment) binds to a vertebrate HMGB A box but does not
specifically bind to non-A box epitopes of HMGB, and inhibits release of
a proinflammatory cytokine from a vertebrate cell treated with an HMGB
protein. A method of treating a condition characterized by activation of
an inflammatory cytokine cascade comprises administering an antibody of
the invention, or its antigen-binding fragment. The condition is selected
from sepsis, allograft rejection, arthritis, asthma, lupus, adult
respiratory distress syndrome, chronic obstructive pulmonary disease,
psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
graft versus host disease inflammatory bowel disease, multiple sclerosis
and cachesia, especially sepsis, arthritis, or lupus. The present
sequence is that of the A box of human HMGB1 ADY85512. An identical
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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120 EDMAKADKARYEREMKTYI PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKI KGEHPGL 120 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTWSAKEKGKF 60 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 0; Gaps 100.0%; Score 215; DB 9; Length 215; 100.0%; Pred. No. 8.2e-195; ive 0; Mismatches 0; Indels C Best Local Similarity 100. Matches 215; Conservative 61 61 Query Match Q Ś 8 8 ò

SKKKKEEEEDEEDEEDEEEEEDEEDEEEDDDDE 215 181

SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180 SIGDVAKKLGEMMINTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

121 121

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completed: April 6, 2006, 10:36:45 ne : 189 secs

Search cor Job time

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

April Run on:

6, 2006, 10:37:03; Search time 41 Seconds (without alignments) 504.551 Million cell updates/sec

US-10-717-984-1

215 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE Title: Perfect score:

Sequence:

215

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

·		oto)			SUMMARIES	
esult No.	COL	Mat	Lengt	BB	1	Description
	215	100.0	ı	7	S02826	nhistone chr
~	206	95.8	215	Н	S01947	nonhistone chromos
m	188	87.4	215	Н	NSRTH1	
4	188	87.4	215	7	I48688	non-histone chromo
Ŋ	143	66.5	170	7	A27853	nonhistone chromos
9	141	65.6	215	7	A28897	nonhistone chromos
7	108	50.2	216	~	S29857	nonhistone chromos
80	29	13.5	172	7	A24019	nonhistone chromos
6	29	13.5	204	7	S48708	high-mobility-grou
10	29	13.5	204	~	T01071	high mobility grou
11	26	12.1	209	H	NSHUH2	stone chi
12	26	12.1	210	7	A34719	nonhistone chromos
13	26	12.1	210	~	S54774	high mobility grou
14	24	11.2	54	~	S68823	HMG1 protein homol
15	22	10.2	205	~	S26062	nonhistone chromos
16	20		210	7	862355	high mobility grou
17	19	8.8	186	~	S30221	nonhistone chromos
18	19		207	7	JC1129	nonhistone chromos
19	19	•	207	7	JC1114	high-mobility grou
20	17	7.9	186	~	B61611	nonhistone chromos
21	17	7.9	792	7	T42963	ᆽ
22	15	7.0	201	7	I50254	HMG-1 - chicken
23	. 15	7.0	202	~	S22359	nonhistone chromos
24	15	7.0	215	~	151067	24
52	15	7.0	387	~	S02708	troponin T - fruit
56	15	7.0	393	7	JC6179	넍
27	15	7.0	393	~	S50068	nonhistone chromos
58	15	7.0	396	~	S13251	troponin T - fruit
59	14	6.5	49	7	D61510	high mobility grou

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Gaps

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9 9

1 MGKGDPKKPRGKOASSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKBKGKF 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL BDWAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL

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1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF

100.0%; Score 215; DB 2; Length 215; larity 100.0%; Pred. No. 1e-179; Conservative 0; Mismatches 0; Indels 0

Query Match Best Local Similarity Matches 215; Conserv

120 120

121 SIGDVAKKIGEMMINITAADDKQPYEKKAAKIKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

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181 SKKKKEEEEDEEDEEDEEDEEDEEDEEEDDDDE 215

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2442 6626 7446 7446 7466 7466 7466 7466	589 589 713 754
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0 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 0 6 4 8

ALIGNMENTS

RESULT 1

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0. U-Dec-1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
R;Wen, L.; Huang, J.K.; July-1221, 1389
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HWG-1.
A;Reference number: S02826; WUID:89160247; PMID:2922262
                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: UNIPROT: P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro A;Reference number: A33178; MUID:91176935; PMID:2079031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GDB:133789; OMIM:163905
A,Exposs-references: GDB:133789; OMIM:163905
A,Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
nonhistone chromosomal protein HMG-1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: protein
A,Residues: 2-13, XXF - KWR>
A,Cross-references: UNIPARC:UPI00001771D7
A,Accession: G33178
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A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UP100001771D7
                                                                                                                                                                                                                                                                                                                                 A, Accession: S02826
A, Molecule type: mRNA
A, Residues: 1-215 < WEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
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6 10:48:15 2006

Thu Apr

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nonhistone chromosomal protein HMG-1 - rat
N'Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A41175; A27299; A30188; B48771; A48771; C48771
R;Mercmides, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-Kba heparin-binding protein of brain (amphoterin) involved in neurite outgro
A;Reference number: A41175; MUID:91358468; PMID:1885601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN::
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
R;Paonessa, G.; Frank, R.; Cortese, R.
A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UP10000173984
A;Cross-references: UNIPARC:UP10000173984
B;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P. J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiParkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala, L. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-KDa protein in a family of HMG1-type polypeptides. Enhanced & A;Reference number: A48771; MUID:93374971; PMID:8366113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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A/Status: preliminary
A/Molecule type: protein
A/Residues: 98-105./x', 107-112 <PA2>
A/Cross-references: UNIPARC:UPI0000173986
A/Cross-references: UNIPARC:UPI0000173986
A/Experimental source: postnatal brain
A/Note: sequence extracted from NUSI backbone (NCBIP:137788)
C/Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C/Reywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental
F;6-83/Domain: HMG box homology cHMG|->
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A30188; MUID:89066894; PMID:2461949
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Best Local Similarity 100.0%; Pred. No. 3.3e-156;
Matches 188; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UP10000173985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-215 <MER>
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                                                                                                                                                                                                                                            Ny Alternate names: 33K protein; HWG-1 - bovine
Ny Alternate names: 33K protein; high-mobility-group protein HMG-1
C; peccies: Bos ptimigenius taurus (catte)
C; pate: 30-8ep-1899 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004
C; Accession: $01947; A61611; $\overline{8}$1059; I45910
R; Kaplan, D.J.; buncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A; Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A; Accession: $01947
A; MUD:89057489; PMID:3194213
A; Accession: $01947
A; MUD:89057489; PMID:3194213
A; Molecule type: mRNA
A; Residues: 1-21s - KAAP
A; Cross-references: UNIPROT:P10103; UNIPARC:UP1000016C31D; EMBL:X12796; NID:416; PIDN:C
R; Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FBBS Lett. 122, 264-270, 1980
A; Reference number: A61611; MUD:81138848; PMID:7202717
A; Accession: A61611
A; Reference number: A61611; MUD:81138848; PMID:7202717
A; Accession: A61611
A; Residues: 2-22, 'S', 24-40; 48-105,'A', 107-157, 'X', 160-193,'D', 195
A; Cross-references: UNIPARC:UP10000173988
B; Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FBBS Lett. 267, 139-141, 1990
A; Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-A; Residues: 210726; MUD:90306387; PMID:2355081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Rocession: S10959
A; Residues: 2-22, Y., 24-38 cCRN-
A; Residues: 2-22, Y., 24-38 cCRN-
A; Residues: 2-22, Y., 24-38 cCRN-
A; Cross-references: UNIPARC: UP10000173989
R; Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1994
A; Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-groun A; Reference number: 145910; MUID:84128872; PMID:6141822
A; Reference number: 145910; MUID:8418872; PMID:6148872; PMID:6148872; PMID:6148872; PMID:6164872; PMID:616
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95.8%; Score 206; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.1e-172;
Matches 206; Conservative 0; Mismatches 0; Indels
SKKKKEEEEDEEDEEDEEDEEDEDEEEDDDE 215
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A Molecule type: mRNA
A Meaidues: 1-212 cfSU.
A Residues: 1-212 cfSU.
A) KResidues: 1-212 cfSU.
A) Cross-references: UNIPROT: P12682; UNIPARC: UPI000016C6C4; GB:M21683; GB:M21684; NID:g16
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords chromosomal protein; DNA binding; nucleus
F; 6-83/Domain: HMG box homology cHMG1.>
F; 92-166/Domain: HMG box homology cHMG2.>
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Sus scrofa domestica (domestic pig)
C,Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                         1 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLP
                                                                                                                                                                                                                                                                                                        46 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF
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                C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DMB binding; nucleus F:1-38[Domain: HMG box homology (fragment) <HMGl> F:47-121/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
                                                                                                                                                                         Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 215;
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R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 x
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
                                                                                                                                                                             Score 143; DB 2; Le
Pred. No. 4.1e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 141; DB 2; Le
Pred. No. 2.7e-115;
                                                                                                                                                                                                       ilarity 100.0%; Pred. No. 4.1
Conservative 0; Mismatches
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Best Local Similarity 100.0%;
Matches 141; Conservative 0;
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Best Local Similarity
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R; Stros, M.; Dixon, G.H.
                                                                                                                                                                                                           Similarity
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A; Residues: 1-216 <STR>
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Best Local Simi
Matches 143;
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non-histone chromosomal high-mobility group 1 protein - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148689; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Fitle: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Reterence number: 148688
A;Reture: preliminary; translated from GB/EMBL/DDBJ
A;Reterence: UNIPROT:P07155; UNIPARC:UP100000008A6; EMBL:Z11997; NID:953381; PIDN
B;Retrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J; Bilo: Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7961836
A;Accession: A555402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: 1189, E7,191-215 <FER>
A;Cross-references: 1-189, E7,191-215 <FER>
A;Cross-references: UNIPARC: UP1000016CDD6; EMBL: X80457; NID:g620097; PIDN: CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Amm. Genome 5, 91-99, 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse H
A;Reference number: 157021; MUID:94235965; PMID:8180479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
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nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
(.)Species Cricetulus griseus (Chinese hamster)
(.)Species Cricetulus griseus (Chinese hamster)
(.)Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
(.)Accession: A27853
Kilee, K.L.D.; Pentecore, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.4%; Score 188; DB 2; L. 100.0%; Pred. No. 3.3e-156; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: 157021
A,Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 100.0
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKKKKEEE 188
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high mobility group protein T - rainbow trout
NiAlternate names: HMG-T protein
Cispecies: Oncorhynchus mykiss (rainbow trout)
Cispecies: Oncorhynchus mykiss (rainbow 12-Peb-1999 #text_change 09-Jul-2004
Ciscession: T01071
Ripertecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high A;Reference number: A24019; MUID:85269614; PMID:4022777
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A,Accession: A42425
A,Golecule type: D0.
A,Rosidues: 2-209 < SHI>
A,Rosidues: 2-209 < SHI>
A,Rosidues: 2-209 < SHI>
A,Cross-references: UNIPROT.P26583; UNIPARC:UPI000012CA25; GB.M83665; NID:G184235; PIDN:JA,Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A,Note: initiator Met not shown
R,Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, Majrile: Sequence of human HMG2 cDNA.
A,File: Sequence of human HMG2 cDNA.
A,Reference number: S20061; MUID:92093633; PMID:1754403
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A;Residues: 1-209 <MAJ>
A;Constrics:
C;Genetics:
A;Gene: GDB:NHCP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P07746; UNIPARC:UPI000012CA3E; EMBL:X02666; NID:g64327; PIDN C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology F;91-165/Domain: HMG box homology <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Dacession: AA4125; Bsoudence revision 31-Mar-1992 #text_change 09-Jul-2004
C;Dacession: A4425; S20061; $18068
R;Shirakawa, H.; Yoshida, M.
J;Blol. Cham. 267; 6641-6645, 1992
J;Blol. Cham. 267; 6641-6645, 1992
A;Fitle: Structure of a gene coding for human HWG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DMA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <PEN>
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            33 ASVNFSEFSKKCSERWKTMSAKEKGKFED 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 ASVNFSEFSKKCSERWKTMSAKEKGKFED 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 ASVNFSBFSKKCSERWKTMSAKEKGKFED 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonhistone chromosomal protein HMG-2 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119451; OMIM:118880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
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Matches
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C.Species: Salmo sp. (trout)
C.Species: Salmo sp. 
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548708
high-mobility-group-1 protein - trout
high-mobility-group-1 protein - trout
C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708
By Stros M.; Nishikawa, S.; Dixon, G.H.
Eur. J. Biochem. 225, 581-591, 1994
A;Title: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference number: S48708; MUID:95045507; PMID:7957172
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                                                                                                                                                                                                                                                                                                                                                                                               PSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-204 «STR>
A; Cross-references: UNIPARC:UDIO0001771D9
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F; 5-82, Domain: HMG box homology «HMG2»
F; 91-165/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 IAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEDEEDEEDE 206
                                                                                                                                                                                                                                          Length 216;
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                                                                                                                                                                                                                                                                                                                  0; Indels
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A24019
nonhistone chromosomal protein HMG-T - trout (fragment)
                                                                                                                                                                                                                                      Query Match
S0.2*; Score 108; DB 2; I
Best Local Similarity 100.0*; Pred. No. 1.5e-86;
Matches 108; Conservative 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 29; Conservative
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Matches 29; Conserval
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Gaps

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Length 54; Indels

DB 2; Le 6.3e-14;

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C;Date: 11.Mar-1998 #sequence revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S26062; S25487; <u>T</u>48408
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.
Nucleic Acids Res: 20, 4927, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the non-histone chromosomal high m. A;Reference number: 148408; MUID:93027215; PMID:1408807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT: P30681; UNIPARC: UPI000016CDD8; EMBL: X67668; NID: 951338; PIDN A;Note: this is a revision to the sequence from reference $25487
S.Folzenburg, F.; Dinkl, E.; Grummt, F.
submitted to the EMBL Data Library, August 1992
A;Reference number: $25487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-183,'KNUSED',190-195,'E',197-198,'ED',201-202,'G',204-205,'EDEE' <STW>
A;Cross-references: UNIPARC:UPI00001771D1; EMBL:X67668
A;Note: this sequence has been revised in reference S26062
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: hmg2
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.2%; Score 22; DB 2; Length 205; Best Local Similarity 100.0%; Pred. No. 1e-11; Matches 22; Conservative 0; Mismatches 0; Indels
F;6-54/Domain: HMG box homology #status atypical <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                     nonhistone chromosomal protein HMG-2 - mouse N;Alternate names: high mobility group 2 protein C;Species: Mus musculus (house mouse)
                                                         Query Match 11.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 6.3 Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                    28 KKKHPDASVNFSEFSKKCSERWKT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GKMSSYAFFVQTCREEHKKKHP 32
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                                                                                                                                                                                           28 KKKHPDASVNFSEFSKKCSERWKT
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A;Residues: 1-205 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S26062
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                          A34719
nonhistone chromosomal protein HMG-2 - pig
C;Species us scrofa domestica (domestic pig)
C;Species 06-Uul-1990 #sequence_revision 06-Uul-1990 #text_change 09-Jul-2004
C;Accession: A34719
R;Shizakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A;Reference number: A34719; MUID:90275208; PMID:2350545
                                                                                                                                                                                                                                                                                                                 A;Accession: A34719
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-210 < SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology < HMG1>
F;92-166/Domain: HMG box homology < HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-210 «ZWI»
A; Residues: 1-210 «ZWI»
A; Rossidues: 1-210 «ZWI»
A; Cross-references: UNIPROT: P30681; UNIPARC: UPI000016432C; EMBL: Z46757; NID: g609168; PIG C; Superfamily: nonhistone chromosomal protein HWG-2; HWG box homology «HWG1»
F; 6-31 Domain: HWG box homology «HWG1»
F; 92-166 / Domain: HWG box homology «HWG2»
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568823
HAGI protein homolog, 6K - mouse
C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 02-Jul-1998
C;Accession: S68823
E;Sparatore, B.; Patrone, M.; Passalacqua, M.; Pontremoli, S.
FEBS. Lett. 386, 95-98, 1996
A;Title: A 6 kDa protein homologous to the N-terminus of the HMG1 protein promoting stim
A;Reference number: S68823; MUID:96228042; PMID:8647297
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S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774, S5211
R;Zwilling, S.; Koenig, H.; Wirth, T.
BMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of
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A;Experimental source: C44 MEL cells
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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A; Status: preliminary; nucleic acid sequence not shown
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Matches 26; Conservative 0; Mismatches
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A; Residues: 1-54 <SPA>
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01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
101-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Name-HWGB1; ORFNames-RP11-550P23.1-004;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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04R844;
13-SEP-2005 (TYEMBLrel. 31, Created)
13-SEP-2005 (TYEMBLrel. 31, Last sequence update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
Testis cDNA clone: QtsA-13487, similar to human high-mobility group
                                                                                                                                                                                                                                                                                                                                                                                 Pelan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AL15348; CA115600.1; -; Genomic_DNA.
GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SEQUENCE 215 AA; 24894 MW; 8A868CF277D417BS CRC64;
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06p4n5
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                                         Q80YZI_MOUSE
Q9NQJ4_HUMAN
HMG2_BOVIN
Q7TP52_MOUSE
Q6NX86_BRARE
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                                                                                                                             Q9CT19_MOUSE
Q96J53_HUMAN
                               XENLA
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QSBKQ1_M
Q9NYD7_H
Q6P4NS_X
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NCBI_TaxID=9606;
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04R844_MACFA
HMG1_CANFA
HMG1_BOVIN
0517C5_HUMAN
054RP9_EAT
0558RP9_EAT
0558RP9_EAT
0568EV5_MOUSE
HMG1_MOUSE
HMG1_RAT
068RM0_MOUSE
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059GM1_HUMAN

HMG1_CRIGR

0577C6_HUMAN

088611_SPAEH

HMG1_PIG

0143Z1_HUMAN

0577C1_HUMAN

088612_SPAEH

06P202_MUUSE

06F202_MUUSE
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Q9PUK9 CHICK
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
The active gene that encodes human high mobility group 1 protein (HMG1) contains introns and maps to chromosome 13.";
Genomics 35:367-371(1996).
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MEDLINE=89160247; PubMed=2922262;
Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                SMART; SM00398; HMG; 2.
PROSITE; PS00359; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
Chromosomal protein; DNA-Dinding; Nuclear protein; Repeat.
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78 HMG box 1.
162 HMG box 2.
214 Asp/Glu-rich (acidic).
24763 MW; B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 214; DB 1; Le 100.0%; Pred. No. 9.7e-184;
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                                                                                                        EMBL; AY135519; AAN11296.1; -; mRNA.
EMBL; AY135521; AAN1319.1; -; Genomic_DNA.
HSSP; POTIS 1 AAB.
SMR; Q6YKA4; 1.83, 92-170.
ENSEMD1; ENSCAFG00000006597; Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P09429; Q6IBB1;
01-MAR-1989 (Rel. 10, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA
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     European Bioinformatics Institute.
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Nucleic Acids Res. 17:1197-1214(1989).
                                                                                                                                                                                                                                       Interpro; IPR000135; Highmoblty 12.
Interpro; IPR000910; HMG 12 box.
Pfam; PF00505; HMG box; 2.
                                                                                                                                                                                                                                                                                                                 PRINTS, PR00886; HIGHMOBLTY12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%;
les 214; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=HMGB1; Synonyms=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
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COMPBIAS
SEQUENCE
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                                                               removed
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HMG1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGDVAKKIGEMWNNTAADDKOPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SIGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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                                                                                                                                                                                                              International consortium for macaque cDNA sequencing, analysis, "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications "; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cannivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MULLOLIGE SEQUENCE [GENOMIC DNA / MRNA].

MULLOLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;

MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;

MULLOLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;

Bullerdiek J., Nolte I.;

"Molecular characterization of the canine HMGB1.";

"Molecular characterization of the canine HMGB1.";

-I- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA (By similarity).

-I- SUBCELLULAR LOCATION: Nuclear (By similarity).

-I- SUBCELLULAR LOCATION: Othe HMG1/HMG2 protein family.

-I- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last amoutation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Evarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                      Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Habhimoto K.; Subaritution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AB166615; BAE00728.1; -; mRNA. SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 215; DB 2; L 100.0%; Pred. No. 1.2e-184;
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Les 215; Conservative
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1 (HMGB1),.
aca fascicularis
                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                 NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECOTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUB-Brain, Cervix, and Testis;

MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Straubberg R.E., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan K.J., Malek J.A., Gunsarten P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeabey W., Helton B. E., Ketteman M., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brown A., Schein J.B., Jones B.J.M., Marra M.A.,

Brown A., Schein J.B., Jones E.D., Marra M.A.,

Brown A., Schein J.B., Jones E.D., Marra M.A.,

Brown A., Schein J.B., Jones E., More C., Hangan A.,

Brown A., Schein J.B., Jones E., Marra M.A.,

Brown A., Schein J.B., Jones E., Welley E.,

Brown A., Schein J.B., Jones E., Jones E., Jones E.,

Brown A., Schein J.B., Jones E., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
EDERT L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
"Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201).",
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Mammary carcinoma;
MEDLINE-97295304; bubMed=9150946;
MEDLINE-97295304; bubMed=9150946;
Stamussen R.K., Ji H., Zeddes J.S., Moritz R.L., Reid G.E.,
Simpson R.J., Dorow D.S.;
Simpson R.J., Dorow D.S.;
"Two-dimenabional electrophoretic analysis of human breast carcinoma proteins: mapping of proteins that bind to the SH3 domain of mixed lineage Kinase MLK2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electrophoresis 18:588-598(1997).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.

Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.

Phelan M., Farmer A.;

"Cloning of human full-length CDSs in BD Creator(TM) system donor
                                                                He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-366083; 015350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606; SUBCELLUIAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the HMG1/HMG2 protein family. SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                TISSUE=Small intestine;
The German cDNA consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 57-64 AND 112-126.
(3)NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
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122 IGDVAKKLGEMANNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                     R GO; GO:0000793; C:condensed chromosome; IDA.
R GO; GO:00008301; F:DNA bending activity; TAS.
R GO; GO:0008134; F:transcription factor binding; TAS.
GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.
GO; GO:0006281; P:DNA recombination; TAS.
R GO; GO:0006281; P:DNA repair; TAS.
R GO; GO:0006281; P:DNA unwinding; NAS.
R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006325; P:establishment and/or maintenance of chromat. . . R GO; GO:0006357; P:regulation of transcription from RNA polyme. . . R InterPro; IPR000135; Highmoblty_12.
R InterPro; IPR0001915; Highmoblty_12.
R Pfam; PF00505; HMG_box; Z.
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PROSITE; PS50118; HMG_BOX_2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding;
Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%; Score 214; DB 1; Length 214; 100.0%; Pred. No. 9.7e-184; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 HMG box 1.
214 AMG box 2.
214 AMF/Glu-rich (acidic).
214 E -> D (in Ref. 5).
24763 MW; B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215
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                                                                                                                                                                                                                                                               IntAct; P09429; -.
Ensembl; ENSG00000189403; Homo sapiens
                                                             -; mRNA.
-; mRNA.
-; mRNA.
-; mRNA.
AY377859; AAQ91389.1;
CR749614; CAH18408.1;
CR7456863; CAG33144.1;
BT0006940; AAP35586.1;
BT0006940; AAP35586.1;
BT00013378; AAH03378.1;
BC003378; AAH03378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00886; HIGHMOBLTY12
                                                                                                                                                      BC066889; AAH66889.1;
BC067732; AAH67732.1;
                                                                                                                                                                                                                                          SMR; P09429; 1-83, 92-170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                            HGNC; HGNC:4983; HMGB1.
                                                                                                                                                                                                                                                                                                                               H-InvDB; HIX0011209; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMG; 2.
                                                                                                                                                                                                 PIR; S02826; S02826
HSSP; P07156; 1NHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMG1 BOVIN
                                                                                                                                                                                                                                                                                                                                                        6390
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DNA BIND
COMPBIAS
CONFLICT
SEQUENCE
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ID HMG1_BC
AC P10103;
DT 01-MAR
DT 13-SEPG-
DE High mc
                                                                                      EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                             EMBL;
EMBL;
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120 121

EMBL; X12597; CAA31110.1; -; mRNA.

removed

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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                                     100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                          KKKKEEEEDEEDEEDEEBEEDE 205
                                                                                                                                                                                                                                                                                                                                                           182 KKKKEEEEDEEDEEDEEDE 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                            QST7CS_HUMAN PRELIMINARY;
ID QST7CS_HUMAN PRELIMINARY;
AC QST7CS;
                                                                                                                                         Local Similarity 100.
8
94 1
185 2
22 105 1
115 1
193 1
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SEQUENCE
DNA_BIND
DNA_BIND
                          COMPBIAS
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                                                                                                                               Query Match
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Matches
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R 1878; PO1156; LNEIN.

R 5MR; PO1000793; C:condensed chromosome; ISS.

GO; GO:0000793; C:condensed chromosome; ISS.

GO; GO:0000793; C:condensed chromosome; ISS.

GO; GO:0006218; F:DNA bending; ISS.

R GO; GO:0006218; P:base-excision repair. DNA ligation; ISS.

GO; GO:0006218; P:base-excision repair. DNA ligation; ISS.

GO; GO:0006268; P:DNA repair; ISS.

R GO; GO:0006268; P:DNA unwinding; ISS.

GO; GO:000625; P:establishment and/or maintenance of chromat. . .; ISS.

GO; GO:001055; P:establishment and/or maintenance of chromat. . .; ISS.

R GO; GO:001055; Highmobity_12.

R InterPro; IPR000310; HMG 12_box.

R Pfam; PF00505; HMG 20x; Z...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
MEDLINE-81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
"The primary structures of non-histone chromosomal proteins HMG 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6; Christen T. Bischoff M., Hobi R., Kuenzle C.C.; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not to other types of Z-DNA."; EBS Lett. 267.139-114(1990).

-I- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- SIMILARITY: Belongs to the HMG1/HMG2 protein family.

-I- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
MEDLINE=84128872; PubMed=6141822;
Pentecost B., Dixon G.H.,
Fontecost B., Dixon G.H.,
mobility-group protein (HMG-1).";
Biosci. Rep. 4:49-57(1984).
                                                                                                                                                      Kaplan D.J., Duncan C.H.; "Full length cDNA sequence for bovine high mobility group 1 (HMG1)
                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovinae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00353; HMG BOX_1; 1.
PROSITE; PS00353; HMG BOX_2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding;
Nuclear protein; Repeat.
INIT_MET
                                                                                                                                                                                     protein.";
Nucleic Acids Res. 16:10375-10375(1988)
                                                                                                           NUCLEOTIDE SEQUENCE (MRNA).
STRAIN=Holstein, TISSUE=Fetal thymus;
MEDLINE=89057489; Pubmed=3194213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X12796; CAA31284.1; -; mRNA.
EMBL; M26110; AAA30567.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 122:264-270(1980)
B1).
Name=HMGB1; Synonyms=HMG1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                              2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL333648; CAI15602.1; -; Genomic_DNA.

EMBL; AL33548; CAI15602.1; -; Genomic_DNA.

EMBL; AL33548; CAI15602.1; -; Genomic_DNA.

GO; GO:0000785; C:chromatin; IEA.

GO; GO:0000367; F:DNA binding; IEA.

GO; GO:0000357; F:DNA binding; IEA.

GO; GO:0000357; F:DNA binding; IEA.

InterPro; IPR000135; Highmobly, 12.

InterPro; IPR000135; Highmobly, 12.

PRINTS; PR00866; HIGHMOBLY12.

SMART; SN00398; HMG; 2.
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                                                                                                                                                                                                                                                                                     Length 214;
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Best Local Similarity 100.0%; Pred. No. 5e-164;
Matches 192; Conservative 0; Mismatches 0; Indels
162 HMG box 1.
162 HMG box 2.
214 Asp/Glu-rich (acidic).
22 C -> S (in Ref. 3).
105 C -> A (in Ref. 3).
119 EHPGL -> PGGGV (in Ref. 2).
119 E -> D (in Ref. 3).
123 E -> D (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment)
Name-HWGB1; ORFYAmmes-RP11-550P23.1-001;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                     95.3%; Score 205; DB 1; Le 100.0%; Pred. No. 1.2e-175;
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STRAINE-EVBN/N; TISSUE-Colon, and Mammary tumor. C3;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J. Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDMAKADKARYEREMKTY I PPKGETKKKFKDDNAPKRPPSAFFLFCSEYRPKI KGEHPGL
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
11-SEP-2005 (TrEMBLrel. 31, Last annotation update)
11-SEP-2005 (TrEMBLrel. 31, Last annotation update)
11-SEP-2005 (TrEMBLrel. 31, Last annotation update)
11-SEP-2005 (TrEMBLrel. 31, Last sequence)
11-Sept mediate thymus cDNA, RIKEN full-
1-Booth enriched library, clone: 0330050N16 product: high mobility group
box 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SIGDVAKKLGEMWINITAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                     87.4%; Score 188; DB 2; Length 215;
100.0%; Pred. No. 2.2e-160;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUE=Kidney;
Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
"Amphoterin is associated with the development of the ki
Submitted (JUN-2008) to the EMBL/GenBank/DDBJ databases.
EMBL, AF276734; AAF82799.1; -; mRNA.
SEQUENCE 215 AA; 24894 FW; 8A868DE266D552B5 CRC64;
    (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 188; Conservative
                                                                                                          Muridae; Murinae; Rattus.
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NCBI_TaxID=10090;
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                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                           NCBI_TaxID=10116;
    13-SEP-2005
                          Amphoterin.
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Q58EV5;
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87 KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEK 146
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                                                                   SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AP07881919; AAC27652.1; -; Genomic_DNA.
R BSPB; P07156; 1NHN.
R GO; GO:0000785; C:chromatin; IEA.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0003677; F:DNA binding; IEA.
R GO; GO:0003677; F:DNA binding; IEA.
R GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
R InterPro; IPR00019; HMG 12_box.
R InterPro; IPR00019; HMG 12_box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDINE-2506.60; PubMed=1121785;; DOI=10.1038/3505500;

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Submitted (APR-2002) to the EmBL; BCO91741; AAH91741; -: mRNA.
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GO:0010235; F:nttric-oxide synthase regulator activity; IDA.
GO:0005815; F:protein binding; IPI.
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GO:0006810; F:transport; IDA. Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., GO; GO:0005615; C:extracellular space; IDA. EMBL; BC094030; AAH94030.1; -; mRNA. EMBL; AK037928; BAC29902.1; -; mRNA. EMBL; AK084841; BAC39289.1; -; mRNA. InterPro; IPR000135; Highmoblty_12. SMR; Q58EV5; 2-84, 93-171. MGI:96113; Hmgbl. NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE MGI;

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MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hmgl-containing sequences.";
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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P63158; P07155; P27109; P27428;
01-APR-1988 (Rel. 07, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                                       Length 215;
                                                                                                                                                                                              0; Indels
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                                                                       PROSITE; PS00353; HWG BOX 1; 1.
PROSITE; PS50118; HWG BOX 2; 2.
SEQUENCE 215 AA; 24894 WW; 8A868DE266D552B5 CRC64;
                                                                                                                                                       87.4%; Score 188; DB 2; L
100.0%; Pred. No. 2.2e-160;
ive 0; Mismatches 0;
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InterPro; IPR000910; HMG 12_box.
ofam: PR00505: HMG box. 2
                    Pfam; PF00505; HMG box; 2. --
PRINTS; PR00886; HIGHMOBLTY12.
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Matches 188; Conservative
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                                                         SM00398; HMG;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
ALISchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Diatchenko L., Marusnia K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L.,
As Diatchenko L.,
As Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
And S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,
Rotterield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T. Generation and initial analysis of more than 15,000 full-length human
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use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG_BOX 2; 2.
Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
-i- SIMILARITY: Belongs to the HMO1/HMC2 protein family.
-i- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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SMR; P63158; 1-83, 92-170.

MGI; MGI: 96513; Hmgbl.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0005815; F:protein binding; IPI.

GO; GO:0006810; P:ntransport; IDA.

InterPro; IPR000135; Highmoblty, 12.

InterPro; IPR000135; Highmoblty, 12.
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D -> E (in Ref. 3).
B3C6A91FD6F1B133 CRC64;
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Pred. No. 1.7e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z11997; CAA78042.1; -; mRNA.
EMBL; W00431; AAA20508.1; -; mRNA.
EMBL; X80457; CAA56631.1; -; Genomic_DNA.
EMBL; BA377; AAA57042.1; -; mRNA.
EMBL; BC006586; AAH06586.1; -; mRNA.
EMBL; BC008565; AAH08565.1; -; mRNA.
EMBL; BC008067; AAH08565.1; -; mRNA.
EMBL; BC085067; AAH83067.1; -; mRNA.
PIR; 148688; 148688.
SMR; P63158; 1-83, 92-170.
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HMG box 1.
HMG box 2.
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PRINTS; PR00886; HIGHMOBLTY12.
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Best Local Similarity
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                                                                                                                                                                                                                                                       P63159; P07155; P27428; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 23, Last sequence update) 01-AUG-1992 (Rel. 23, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) High mobility group protein 1 (HWG-1) (High mobility group protein 1 (HWG-1) (High mobility group protein 1) (Amphoterin) (Heparin-binding protein p30). Name=Hmgbl; Synonyms=Hmg-1, Hmgl; Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 1-20.
MEDLINE-89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
                       GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                              GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                     DMAKADKARYEREMKTYI PPKGETKKKPKDPNAPKRPPSAFFLFCSEYRPKI KGEHPGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91358468; PubMed=1885601;
Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
"30-kDa heparin-binding protein of brain (amphoterin) involved in
neurite outgrowth. Amino acid sequence and localization in the
filopodia of the advancing plasma membrane.";
J. Biol. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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MEDLINE=93233672; PubMed=8467791;
Their H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
Thomas J.O.;
 0; Indels
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NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88067717; PubMed=3684582;
Paonessa G., Frank R., Cortees R.;
"Nucleotide sequence of rat liver HMG1 cDNA.";
"Muclaic Acids Res. 15:9077-9077(1987).
                                                                                                                                                                                                                                                   214 AA
 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley, TISSUE=Liver;
                                                                                                                                                                                                                                                   PRT;
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Matches 187; Conservative
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                                                                                                                                                                KKKKEEE 188
                                                                                                                                                                                       KKKKEEE 187
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                     Thomas J.O., Laue E.D.; "Structure of the A-domain of HMG1 and its interaction with DNA as studied by heteronuclear three- and four-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
-!- SIMILARITY: Belongs to the HMG1/HMG2 procein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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"Structure of the HMG box motif in the B-domain of HMG1."; EMBO J. 12:1311-1319(1993).
                                                                                                                         STRAIN=Sprague-Dawley;
MEDLINE=96118376; PubMed=8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue E.D.;
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Asp/Glu-rich (acidic)
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PDB; IHME; NMR; @=88-164.

PDB; IHMF; NMR; @=88-164.

SMR; P63159; 1-83, 92-170.

Ensembl; ENSKNOG00000030351; Rattus norvegicus.

RGD; 2802; Hmgbl.
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BC081839; AAH81839.1; -; mRNA.
BC088402; AAH88402.1; -; mRNA.
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InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
SMRART; SM00398; HMG; 2.
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EMBL; Y00463; CAA68526.1; -; mRNA.
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PROSITE; PS50118; HMG_BOX_2; 2.
                                                                                               STRUCTURE BY NMR OF 1-83.
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PDB; 1AAB; NMR; @=1-83.
PDB; 1CKT; X-ray; A=7-7
PDB; 1HME; NWR; @=88-16.
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                                          DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
                                                                                                IGDVAKKI.GEMWINTAADDKQPYEKKAAKI.KEKYBKDIAAYRAKGKPDAAKKGVVKAEKS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubil F., Suzuki R., Tomita M., Magner L., Washio T., Schriml L.M., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Buwaka K., Marion B., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Satok K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hansegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body CDNA, RIKEN full-length enriched library, clone:C430013M12 product:high mobility group box 1, full insert sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                      181 AA.
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STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
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QBBNMO;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Rukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Karihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Karihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Saito R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Saski D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Tokani M., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
REBBL, AKOB202; BAC38678.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                      MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sunbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sunbata W., Itoh M., Aizawa M., Hazama M., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riks Integrated sequence M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN Integrated sequence analysis (RISA) system-184-format Genome Res. 10:1757-1771(2000).
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SMR; QBENMO; 2-84, 93-171.

SMR; QG1:196113; Hmgpl.

GO; GO:0005634; C:nactellular space; IDA.

GO; GO:0005515; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0005515; F:nitric oxide blosynthesis; IDA.

GO; GO:0006810; P:nitric oxide blosynthesis; IDA.

GO; GO:0006810; P:transport; IDA.

InterPro; IPR000135; Highmoblty 12.

InterPro; IPR000135; Highmoblty 12.

InterPro; IPR000135; Highmoblty 12.
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100.0%; Pred. No. 3.6e-154;
ive 0; Mismatches 0;
STRAIN=C57BL/6J; TISSUE=Whole body;
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PROSITE; PS50118; HMG BOX 2; 2.
NON TER 181
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SM00398; HMG; 2.
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Best Local Similarity 100.(
Matches 181; Conservative
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Carallouine Schinagawa A., Schipata K., Yoshino M., Itch M., Ishini Y.,

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                                                                                               OBC7C4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:C920030E14 product:high mobility group
hox 1, full insert sequence. (Fragment).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Forno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Pubbraction of Cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=9927923; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
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"Functional annotation of a full-length mouse cDNA collection.";
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STRAIN=C57BL/6J; TISSUE=Thymus;
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                                                                                     QEC7C4 MOUSE PRELIMINARY;
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61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamananto R., Matsunato H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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WGI; MGI:96113; Hmgbl.
GO; GO:0005615; Cactracellular space; IDA.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005515; F:nitric-oxide synthase regulator activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006810; P:nitric oxide biosynthesis; IDA.
GO; GO:0006810; P:transport; IDA.
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Last annotation update)
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100.0%; Pred. No. 1.7e-151;
iive 0; Mismatches 0;
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HSSP; P07156; 1NHN.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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InterPro; IPR000910; HMG 12 box.
Pfam; PF00505; HMG box; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00886; HIGHMOBLTY12.
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Q9QX40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liee K.-L.D., Lum H.-K., Nevo E.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
REL; AFO78820; AAC27653.2; -; Genomic_DNA.
RSP; P07156; 1NHN.
RSP; P07156; 1NHN.
RO; GO:000548; C:chromatin; IEA.
RO; GO:000547; F:DNA binding; IEA.
RO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
RO; GO:000635; P:regulation of transcription, DNA-dependent; IEA.
RO; GO:0006515; P:RONOB10; Highmoblty_12.
RITHERPOST; PRO00135; Highmoblty_12.
REPROFICE: REGULATION OF TRANSCRIPTION, REPROFICE: REGULATION, REPROFICE: REGULATION, REPROFICE: REGULATION OF TRANSCRIPTION, REPROFICE: REGULATION OF TRANSCRIPTION OF TRANSCRIP
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
101-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment).
Name=HMGB1; ORFNames=RP11-550P23.1-009;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; ALJ53648; CAIJ5604.1; -; Genomic_DNA.

EMBL; ALJ53648; CAIJ5604.1; -; Genomic_DNA.

EMBL; ALJ53648; CAIJ5604.1; -; Genomic_DNA.

SMR; OST7022; 2-844, 98-157.

R GO; GO:00005634; C:nucleus; IEA.

GO; GO:00005634; C:nucleus; IEA.

R GO; GO:0000535; F:nucleus; IEA.

R GO; GO:0000535; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R Pfam; PF000565; HMG box; Z.

R Pfam; SM00386; HMG box; Z.

R PROSITE; PS00139; HMG; Z.

R PROSITE; PS00139; HMG; Z.

R PROSITE; PS00118; HMG; Z.
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Pred. No. 3e-135;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00153; HWG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24895 MW; 599FBBA6FDF41F17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 VKAEKSKKKKEEEEDEEDEEEEEDEEDEEDEDDDB 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKAEKSKKKKEEEEDBEDEEDEEBEEEEBDEEDEEBEDDDE 215
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100.0%; Pred. No. ...
0; Mismatches
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Muridae; Spalacinae; Nannospalax
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QST7C2;
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                                                                                                                            NUCLEOTIDE SEQUENCE
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OST77C2 HUM
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DT 01-FE
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earch completed: April 6, 2006, 10:40:42 ob time : 231 secs

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US-09-538-092-883
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US-09-214-881A-1
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Sequence 4, Appli
Sequence 7904, Appli
Sequence 10813, A
Sequence 4826, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 10728, Appli
Sequence 11, Appli
Sequence 13, Appli
Sequence 11, Appli
                                                                           April 6, 2006, 10:40:58 ; Search time 46 Seconds (without alignments) 386.419 Million cell updates/sec
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                                                                                                                          US-10-717-984-1
215
1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEBEEDDDDB
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                         Issued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-538-092-883
US-09-214-881A-1
US-09-214-881A-3
US-09-214-881A-4
US-09-214-881A-5
US-09-513-999C-4824
US-09-513-999C-4824
US-09-513-999C-4826
US-09-513-999C-4826
US-09-513-999C-4826
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US-09-513-999C-4826
US-09-513-999C-4826
US-09-214-881A-2
US-09-214-881A-1
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                        - protein search, using sw model
                                                                                                                                                                         OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                            Searched:
                                                                                                                                                     Sequence:
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Sequence 8, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 124, Appli
Sequence 324, Appli
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## Sequence 883, Application US/09538092

## Patent No. 6753314

## GENERAL INFORMATION:

## APPLICANT: Giot, Loic

## APPLICANT: Mansfield, Traci A.

## TILE OF INVENTION:

## PILE REFERENCE: 15966-542

## CURRENT APPLICATION NUMBER: US/09/538,092

## CURRENT PILING DATE: 2000-03-29

## PRIOR APPLICATION NUMBER: 60/127,352

## PRIOR PILING DATE: 2000-02-01

## PRIOR PILING DATE: 2000-02-01

## NUMBER OF SEQ ID NOS: 1387

## SOFTWARE: CuraPatSeqFormatter Version 0.9

## SEQ ID NO 803

## SEC ID NO 803

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LCATTON: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-902-883-092-89
US-08-469-526A-8
US-08-734-591A-8
US-08-470-335-8
US-08-734-664A-8
US-08-734-664A-8
US-08-770-339-8
US-08-4770-339-8
PCT-US94-605087C-8
PCT-US94-605087C-8
PCT-US94-605087C-8
US-09-513-999C-4966
US-09-735-457-324
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ORGANISM: Homo sapiens
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Matches 205; Conservative
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                                                                                                 APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Useugi, Hiroko
APPLICANT: Useugi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
APPLICANT: Osakada, Fumio
APPLICANT: Osakada, Fumio
APPLICANT: Osakada, 191600511C DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 214
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APPLICANT: Sobajima, Junko
APPLICANT: Useudi, Hiroko
APPLICANT: Useudi, Hiroko
APPLICANT: Useudi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
APPLICANT: Osakada, Funio
APPLICANT: Osakada, Funio
APPLICANT: Usenda, Michiteru
APPLICANT: Osakada, Funio
APPLICANT: Usenda, Michiteru
APPLICANT: Usenda, Juliana, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 214; DB 2; Length 214; 100.0%; Pred. No. 2.6e-187; ive 0; Mismatches 0; Indel8
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Sequence 1, Application US/09214881A
Patent No. 6822078
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Patent No. 6822078
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ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: Bos taurus
US-09-214-881A-3
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Best Local Similarity

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61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120
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                                              GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE
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Gaps
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### APPLICANT Sobajim Junko
### APPLICANT Ucasuji, Hiroko
### APPLICANT Tanaki, Masao
### APPLICANT Tanaki, Masao
### APPLICANT Tanaki, Masao
### APPLICANT Shirakawa, Hitoshi
### APPLICANT Shirakawa, Hitoshi
### APPLICANT Shirakawa, Hitoshi
### APPLICANT Osakada, Fumio
### TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
### PERENCE: 068983.0104
### CURRENT PILLING DATE: 1999-06-07
### SOFTRANE: Patentin Ver. 2.1
### SEQ ID NOS: 13
### SEQ ID NOS: 13
### SEQ ID NOS: 17
### TYPE: P##
### TYPE: P##
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0; Indels
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Pred No. 7.1e-120;
0; Mismatches
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US-09-214-881A-5
US-09-514-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
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Sobajima, Junko
Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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, ORGANISM: Human
US-09-949-016-10813
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Batent No. 6783961

GENERAL INPORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NOWBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7904
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APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osaskada, Funio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEG ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                 Query Match 65.1%; Score 140; DB 2; Length 214; Best Local Similarity 100.0%; Pred. No. 7.1e-120; Matches 140; Conservative 0; Mismatches 0; Indels
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ORGANISM: Rattus rattus
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7904
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Matches 98; Conserv
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US-09-949-016-10813
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US-09-513-999C-7904
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LENGTH: 214
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10013

LENGTH: 213
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4824
LENGTH: 110
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Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 90; Conservative 0; Mismatches 0; Indels
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Pred. No. 3.9e-76;
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100.0%; Pred. No. s...
0; Mismatches
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Patent No. 6783961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE
CACATION: 91
CHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824
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Best Local Similarity 100.0
Watches 92; Conservative
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Sequence 1, Application US/08803545
Patent No. 5851986
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 30; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
US-09-513-999C-4826
                                                                                                                                                                                                                                                                              US-08-803-545-1
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; Sequence 4826, Application US/09513999C
; Retent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US /09/513,999C
; CURRENT PILING DATE: 2000-02-26
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4826
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
                            Sequence 4825, Application US/09513999C
; Batent No. 6783961
; Batent No. 6783961
; GENERAL INOFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REPRENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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28.4%; Score 61; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 4e-48;
Matches 61; Conservative 0; Mismatches 0; Indels
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NAME/KEY: UNSURE
LOCATION: 17
OTHER INFORMATION: Xaa=Ala or Gly
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COTHER INFORMATION: Xaa=Asp or Gly US-09-513-999C-4825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa=Glu or Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa=Lys or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: UNSURE
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NAME/KEY: UNSURE
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                US-09-513-999C-4825
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LENGTH: 110
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Sequence 1018, Application US/09538092
Fatent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; FILE REFERENCE: 15966-542
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APPLICANT: YAMAMURA, Junichi
APPLICANT: YAMAMURA, Junichi
APPLICANT: GOTO, Massaki
APPLICANT: GOTO, Massaki
APPLICANT: AOE, Selichiro
TITLE OF INVENTION: Inhibiting Bone Resorption
VIMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teeta, Hurwitz & Thibeault
STREET: 125 High St.
Query Match 18.1%; Score 39; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 2.7e-28; Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 30; 2.5e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: 02110
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,545
TILING ADDITE: 20-FEB-1997
TILING ADDITE: 20-FEB-1997
TILING ADDITE: 20-FEB-1997
                                                                                                          1 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 39
                                                                                  52 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 90
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Yoshida, Michiteru
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Best Local Similarity 100.0
Matches 26; Conservative
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ORGANISM: Rattus rattus
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SEQ ID NO 8
LENGTH: 209
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APPLICANT: Ocaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
APPLICANT: Osabada, Funio
APPLICANT: Osabada, Funio
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osabada, Funion
APPLICANT: Shirakawa, Hitoshi
APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.1%; Score 26; DB 2; Length 208; Best Local Similarity 100.0%; Pred. No. 5.3e-16; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P26583 US-09-538-092-1018
CURRENT APPLICATION NUMBER: US/09/538,092;
CURRENT FILING DATE: 2000-03-29;
PRIOR APPLICATION NUMBER: 60/127,352;
PRIOR FILING DATE: 1999-04-01;
PRIOR PILING DATE: 1999-04-01;
PRIOR PILING DATE: 2000-02-01;
NUMBER OF SEQ ID NOS: 1387;
SOFTWARE: CURAPAtSeqFormatter Version 0.9;
SOFTWARE: CURAPATSEGFORMATER VERSION 0.9;
LENGTH: 208
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Sobajima, Junko
Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-09-214-881A-2
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GENERAL INFORMATION:
APPLICANT: Ozaki, S
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SEQ ID NO 2
LENGTH: 208
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US-09-214-881A-6
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Junko
APPLICANT: Obasjima, Junko
APPLICANT: Obaszaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Tokaka, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: 068383.0104
CURRENT APPLICATION NUMBER: 1999-06-07
KURBENT FILING DATE: 1999-06-07
KORRENT FILING DATE: 1999-06-07
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APPLICANT: STATEMAN, Hitching APPLICANT: STATEMAN, HITCHING APPLICANT: STATEMAN, HITCHING APPLICANT: OSARda, Fumio TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES FILE REFERENCE: 0608383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 209
TYPE: PRT
ORGANISM: SUS SCROÍA
                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 26; DB 2; Length 209; Best Local Similarity 100.0%; Pred. No. 5.3e-16; Matches 26; Conservative 0; Mismatches 0; Indels
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Pred. No. 5.3e-16;
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100.0%; Pred. No. ...
0; Mismatches
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Job time : 47 secs
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Patent No. 6822078
GENERAL INFORMATION:
APPLICANT: OZAKI, Shoichi
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Sequence 37, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1757, Appl
Sequence 1757, Appl
Sequence 1055, Ap
Sequence 6757, Ap
Sequence 18, Appl
Sequence 10, Appl
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; Sequence 1446, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Brighlard, Eric K.
; TITLE OF INVENTION: CANCER
; TITLE OF INVENTION: CANCER
; FILE REPERBRICE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR PELICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOGTWARE: FREESEQ for Windows Version 4.0
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                 US-10-938-992-37
US-09-214-681A-4
US-09-214-681A-5
US-10-726-195-4
US-11-0726-195-4
US-11-013-684-17
US-09-925-390-1757
US-09-925-299-1055
US-10-106-698-6757
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US-10-456-947-6
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  ORGANISM: Homo sapiens
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US-10-087-192-1446
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537.924 Million cell updates/sec
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1 MGKGDPKKPRGKMSSYAFFV......DEEEEEDEEDEDEEEDDDDE
                                                                                                                                                 April 6, 2006, 10:41:43 ; Search time 167 Seconds
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-147-447-1
US-10-456-949-1
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Maximum DB seq length: 200000000
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ORGANISM: Homo Sapien
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| Sequence 1, Application US_10300072
| Publication No. US_20030144201A1
| GENERAL INFORMATION:
| APPLICANT: Kevin J. Tracey
| APPLICANT: Howland Shaw Warren, Jr.
| APPLICANT: Mitchell P. Fink
| TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
| TITLE OF INVENTION: AGENTS
| FILE REFERENCE: 3268.1001.005
| CURRENT PILING DATE: 2002-11-20
| PRIOR PAPLICATION NUMBER: US_10/147,447
| PRIOR PELING DATE: 2001-05-15
| PRIOR PELING DATE: 2001-05-15
| PRIOR PELING DATE: 2001-05-15
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: PEREERG for Windows Version 4.0
| TENGRAL OF SEQ ID NOS: 58
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100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6e-173;
tive 0; Mismatches 0;
                  APPLICANT: Yang, Huan
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Fink, Mitchell P.
TITLE OF INVENTION: Use of HMG Fragments as
ITILE OF INVENTION: Anti-Inflammatory Agents
FILE REFERENCE: 3268.1001-001
CURRENT APPLICATION NUMBER: US/10/147,447
CURRENT PILING DATE: 2002-08-16
PRIOR PEDIA APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 215
APPLICANT: Tracey, Kevin J.
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: HMIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: HMTL-INFLAMMATORY AGENTS

TITLE OF INVENTION: MMTL-INFLAMMATORY AGENTS

FILE REFERENCE: 3268.1001-007

CURRENT APPLICATION NUMBER: US/10/456,947

PRIOR APPLICATION NUMBER: 10/147,447
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100.0%; Score 215; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0;
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APPLICANT: Revin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
TITLE OF INVENTION: USE OF HMG FRAGMENTS
FILE REFERENCE: 3269.1001-006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FARESEQ for Windows Version 4.0
LENGTH: 215
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Publication No. US20040005316A1
GENERAL INFORMATION:
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Publication No. US20050032697A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al.
TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28667/39359A
CURRENT APPLICATION NUMBER: US/10/868,577A
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
LENGTH: 215
                                  US-10-17,-984-1

Sequence 1, Application US/10717984

Publication No. US20040156851A1

GENERAL INFORMATION:

APPLICANT: Newman, Walter

TITLE OF INVENTION: HMGBI COMBINATION THERAPIES

FILE REFERENCE: 3258.1008-001

CURRENT FILING DATE: 2003-11-20

FRIOR APPLICATION NUMBER: 60/427,846

PRIOR PLING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1
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100.0%; Score 215; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0;
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0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 215; Conservative 0;
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ORGANISM: Homo sapiens
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Publication No. US20040141948A1
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                           0; Mismatches
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 215
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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PUblication No. US20050043235A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al.

ITILE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY

FILE REFERENCE: 28967/39117A

CURRENT APPLICATION NUMBER: US 60/478,114

PRIOR APPLICATION NUMBER: US 60/478,114

PRIOR APPLICATION NUMBER: US 60/478,390

PRIOR APPLICATION NUMBER: US 60/478,390

PRIOR FILING DATE: 2003-06-12

PRIOR FILING DATE: 2003-06-12

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT FILING DATE: 2004-09-10
PRIOR FILING DATE: 2003-09-11
NUMBER OF SEQ ID NOS: 76
SEQ ID NO 74
SEQ ID NO 74
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GENERAL INFORMATION: APPLICANT: Newman, Walter
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ORGANISM: Homo sapiens
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US-10-868-549-22
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LENGTH: 215
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APPLICANT: Sobajina, Junko
APPLICANT: Okacaki, Takahiro
APPLICANT: Tanaka, Macao
APPLICANT: Tanaka, Macao
APPLICANT: Tanaka, Macao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
ITILE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: 06838.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
LENGTH: 214
TYPE: PPP
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; ORGANISM: Homo sapiens
US-10-938-992-74
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Sequence 3, Application US/09214881A, Patent No. US2002009749A1, GENERAL INFORMATION: APPLICANT: Ozaki, Shoichi APPLICANT: Sobajima, Junko
Query Match
Best Local Similarity 100.0
Matches 214; Conservative
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US-10-938-992-38
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                                                                    APPLICANT: Osbail Minko
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Useugi, Hiroko
APPLICANT: Useugi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osbada, Punko
TITLE OF INVENTION: UNABUSIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068393.0104
CURRENT APPLICATION NUMBER: US/10/726,195
CURRENT FILING DATE: 2003-12-02
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEO ID NOS: 13
SOOTWART: Patentin Ver: 2.1
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| Publication No. US20050152903A1 |
| GENERAL INFORMATION: |
| APPLICANT: Newman, Walter |
| APPLICANT: O'NEGE, Theresa |
| APPLICANT: O'NEGE, Theresa |
| APPLICANT: O'NEOFT |
| TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1 |
| FILE REFERENCE: 3258-1033-004-09-10 |
| FILE REFERENCE: 3258-1033-004-09-10 |
| PRIOR FILING DATE: 2003-09-11 |
| NUMBER OF SEQ ID NOS: 76 |
| SOFTWARE: PARESEQ for Windows Version 4.0 |
| LENGTH: 221
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              ; Sequence 1, Application US/10726195; Publication No. US20040229279A1; GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 214; Conserval
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US-10-938-992-40
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LENGTH: 214
  US-10-726-195-1
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99.5%; Score 214; DB 5; Length 221; 100.0%; Pred. No. 4.3e-172; ive 0; Mismatches 0; Indels
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; Sequence 38, Application No. US20050152903A1
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Oin, Shixin
; APPLICANT: Oin, Shixin
; APPLICANT: Oin, Shixin
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; TITLE OF INVENTION: MOSCOORD
; CURRENT FILING DATE: 2004-09-10
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LEASTH: 215
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121 IGDVAKKLGEMMNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180
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APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Masuwa
APPLICANT: Nakao, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Orakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPREBRÜCE: 069383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 3
LENGTH: 214
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CORGANISM: Bos taurus
US-09-214-881A-3
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US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1
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Best Local Similarity 100.
Matches 215; Conservative
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ORGANISM: Homo sapiens
US-10-821-234-1443
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9681, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Seq
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1 MGKGDPKKPRGKWSSYAFFV.....DEBEBEBDBBBEBDDDB
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1: /SIDS5/ptcdata/2/pubpaa/US08 NEW PUB.pep:*
2: /SIDS5/ptcdata/2/pubpaa/US07 NEW PUB.pep:*
3: /SIDS5/ptcdata/2/pubpaa/US07 NEW PUB.pep:*
4: /SIDS5/ptcdata/2/pubpaa/PCT_NEW PUB.pep:*
5: /SIDS5/ptcdata/2/pubpaa/US09 NEW PUB.pep:*
6: /SIDS5/ptcdata/2/pubpaa/US10 NEW PUB.pep:*
7: /SIDS5/ptcdata/2/pubpaa/US10 NEW PUB.pep:*
8: /SIDS5/ptcdata/2/pubpaa/US11 NEW PUB.pep:*
                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-821-234-1443

US-11-186-422-11

US-11-186-422-12

US-11-186-422-13

US-11-166-422-13

US-11-166-422-13

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US-11-166-422-13

US-11-186-422-13

US-11-186-422-13

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US-11-186-422-13

US-11-019-150-4

US-11-044-899-30

US-11-044-899-30

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US-11-044-899-30

US-11-044-899-30

US-11-096-568A-6675

US-11-096-568A-9681

US-11-096-568A-9681

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US-11-096-568A-3681

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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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No.
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Sequence 1443, Application US/10821234

Sequence 1443, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TILE OF INVENTY APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR FILING DATE: 2003-04-07

NUMBER: OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_Genes Version 1.0

SEQ ID NO 1443

LENGTH: 215
Sequence 1564, Ap Sequence 31073, Ap Sequence 9185, Ap Sequence 1554, Ap Sequence 1554, Ap Sequence 1511, Ap Sequence 1565, Ap Sequence 1566, Ap Sequence 1566, Ap Sequence 2770, Ap Sequence 9617, Ap Sequence 9617, Ap Sequence 9517, Ap Sequence 9517, Ap Sequence 9517, Ap Sequence 9517, Ap Sequence 2688, Ap Sequence 26888, Ap Sequence 268888, Ap Sequence 26888, Ap Sequence 26888, Ap Sequence 26888, Ap Sequence 26888, Ap Sequ
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                                                                                US-11-087-099-9185
US-11-087-099-9185
US-10-81-234-1254
US-11-172-740-1569
US-11-172-740-1571
US-11-172-740-1571
US-11-172-740-1566
US-11-172-740-1566
US-11-172-740-1570
US-11-087-099-9017
US-11-096-568A-9680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKKKKEEEEDBEDEEDEEDEEDEEDEEDDDE 215
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121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                       61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                                                                                                                            121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.1%; Score 69; DB 7; Length 69; Best Local Similarity 100.0%; Pred. No. 2.8e-57; Matches 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10719150;
Sequence 6, Application US/10719150;
Publication No. US20040120953A1
GENERAL INNCRMATION:
APPLICANT: Haichao Wang
TITLE OF INVENTION: ANTACONISTS OF HMG1 FOR TREATING
TITLE OF INVENTION: INFLAMMATORY CONDITIONS;
FILE REFERENCE: 3268.1000-011
CURRENT APPLICATION NUMBER: US/10/719,150
CURRENT APPLICATION NUMBER: US/10/719,150
FRIOR PRILING DATE: 2002-11-20
FRIOR PELLING DATE: 2002-01-31
FRIOR FILING DATE: 2002-07-31
FRIOR FILING DATE: 2002-07-31
FRIOR RELING DATE: 2002-07-31
FRIOR FILING DATE: 1999-02-11
FRIOR FILING DATE: 1999-02-11
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                          USECULE 186-422-14

Sequence 14, Application US/11186422

Publication No. US20060057679A1

GENERAL INFORMATION:

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: O'Reefe, Theresa

APPLICANT: Luciano, Peter

APPLICANT: Luciano, Peter

APPLICANT: Oin, Shixin

TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES

FILE REFERENCE: 3258.1021-003

CURRENT FILING DATE: 2005-07-20

FRIOR APPLICATION NUMBER: 60/589,678

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
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61 EKYEKDIAA 69
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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87.4%; Score 188; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-167;
Matches 188; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 215; DB 7; Length 2: Best Local Similarity 100.0%; Pred. No. 1.3e-192; Matches 215; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REPERENCE: 3258.1021.003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 215
LENGTH: 215
TYPE: PRT
US-11-186-422-11
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US-11-186-422-12
| US-11-186-422-12
| US-11-186-422-12
| US-11-186-422-12
| US-11-186-422-12
| US-11-186-422-13
| US-11-186-422-13
| US-11-186-422-13
| GENERAL INFORMATION:
| APPLICANT: Critical Therapeutics, Inc.
| APPLICANT: O'Keefe, Theresa
| APPLICANT: Qin, Shixin
| TITLE OF INVENTION: BAGE PROTEIN DERIVATIVES
| FILE REFERENCE: 328-1021-003
| CURRENT PAPLICATION NUMBER: 2005-07-20
| PRIOR PILING DATE: 2005-07-20
| PRIOR APPLICATION NUMBER: 60/589,678
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: FRASEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 12
LENGTH: 215
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-186-422-12
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                                                                                            Sequence 1234, Application US/10821234

| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Labat, Ivan
| APPLICANT: Adarmani, Susan
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| APPLICANT: APPLICANTION: Methods for Diagnosis and Treatment of Precelampsia
| TITLE OF INVERTION: Methods for Diagnosis and Treatment of Precelampsia
| TITLE OF INVERTION: Methods for Diagnosis and Treatment of Precelampsia
| TITLE OF INVERTION: Methods for Diagnosis and Treatment of Precelampsia
| TITLE OF INVERTION NUMBER: US/10/821,234
| CURRENT APPLICATION NUMBER: US 60/462,047
| PRIOR PILING DATE: 2003-04-07
| NUMBER OF SEQ ID NOS: 1704
| SEQ ID NOS: 1704
| SEQ ID NOS: 1704
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    LOCATION: (1) ... (169)
    COTHER INFORMATION: Xaa = any amino acid or nothing
    (105-10-821-234-1234)

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9.3%; Score 20; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.5%; Score 14; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10719150
Sequence 1, Application US/10719150
Sequence 1, Application Wo. US20040120953A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Haichao Wang
TITLE OF INVENTION: APPLICANT (NITLE OF INVENTION: INFLAMMATORY CONDITIONS
FILE REFERENCE: 3268.1000-011
CURRENT FILING DATE: 2003-11-21
FRIOR APPLICATION NUMBER: US/10/719,150
CURRENT FILING DATE: 2003-11-20
FRIOR APPLICATION NUMBER: US/10/300,068
FRIOR PILING DATE: 2002-07-31
FRIOR PILING DATE: 2000-07-31
FRIOR PILING DATE: 2000-07-31
FRIOR FILING DATE: 2000-07-31
FRIOR FILING DATE: 2000-07-31
FRIOR FILING DATE: 2000-02-14
FRIOR FILING DATE: 2000-02-14
FRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 6
SOFUTHARE: FRAEESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSYAFFVQTCREEHKKKHPD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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CURRENT APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SEQ TWARE: PATENTIN VETSION 3.2
SEQ TWARE: 879
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                                                                                                                                                                32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET
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                                                     DB 6; Length 54;
2e-43;
thes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 54; DB 7; Length 54; 100.0%; Pred. No. 2e-43; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         Publication No. US20060057679A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Luciano, Peter
APPLICANT: Luciano, Peter
APPLICANT: Unit Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
FRIOR FILING DATE: 2005-07-20
FRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FREESEQ for Windows Version 4.0
                                                  25.1%; Score 54; DB (100.0%; Pred. No. 2e-1ive 0; Mismatches
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                                                     Query Match
Best Local Similarity 100.0
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 54; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 22; Conserva
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US-10-719-150-6
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LENGTH: 54
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APPLICANT: SCHWAD, M.

APPLICANT: CHAMA, M.

APPLICANT: CHAMA, M.

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

FILE REPREBUCE: 10200-017-999

CURRENT APPLICATION NUMBER: US/11/044,899

CURRENT FILING DATE: 2001-026

PRIOR PELLING DATE: 2001-09-24

PRIOR PELLING DATE: 2001-09-24

PRIOR PELLING DATE: 1999-11-05

PRIOR PELLING DATE: 1999-11-06

NUMBER OF SEQ ID NOS: 51

LENGTH: 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12397, Application US/11087099
Publication No. US20060041961A1
RENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13; DB 7; Le
Pred. No. 0.00061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(1163) at all Xaa position corner INFORMATION: Xaa = any amino acid US-11-044-899-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-096-568A-28367
; Sequence 28367, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
                                                                                                                             US-11-044-899-30
. Sequence 30, Application US/11044899
. Publication No. US20050260616A1
. GENERAL INFORMATION:
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US-11-087-099-12397
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Best Local Similarity 100.0
Matches 13, Conservative
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33 EDEEDEEEEDEE 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-087-099-12397
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## Sequence 2, Application US/11044899
## Publication No. US20050260616A1
## CAPLICANT: Schwab, M.
## APPLICANT: Schwab, M.
## APPLICANT: Schwab, M.
## TITLE OF INVENTION: THEREON
## TITLE OF INVENTION: THEREON
## TITLE OF INVENTION: THEREON
## FILE REFERENCE: 10200-017-999
## CURRENT APPLICATION NUMBER: US/11/044,899
## CURRENT APPLICATION NUMBER: US/930,972
## PRIOR PPLICATION NUMBER: PCT/US99/26160
## PRIOR PPLICATION NUMBER: PCT/US99/26160
## PRIOR APPLICATION NUMBER: 60/107,446
## PRIOR PPLICATION NUMBER: 51998-11-06
## PRIOR PPLICATION NUMBER: 51998-11-06
## PRIOR PPLICATION NUMBER: 60/107,446
## PRIOR PRIOR PPLICATION NUMBER: 60/107,446
## PRIOR PPLICATION NUMBER: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.5%; Score 14; DB 6; Length 15; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                            Sequence 4, Application US/10719150
; Sequence 4, Application No. US20040120953A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTAGONISTS OF HWG1 FOR TREATING
; TITLE OF INVENTION: INFLAWATORY CONDITIONS
; FILE REFERENCE: 3268.1000-011
; CURRENT APPLICATION NUMBER: US/10/719,150
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/300,068
; PRIOR FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: antigen
US-10-719-150-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 28867
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6675, Application US/11096568A

Sequence 6675, Application No. US20060048240A1

Fublication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: 2750-1552PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 6675

LENGTH: 106
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LOCATION: (1)...(106)

CTHER INFORMATION: Ceres Seq. ID no. 14316260

US-11-096-5688-6675
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

LOCATION: (1)..(447)

CTHER INFORMATION: Ceres Seq. ID no. 2715782

US-11-096-568A-28367
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                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Arabidopsis thaliana
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Matches 10; Conservative
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ORGANISM: Glycine max
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US-11-096-568A-6675
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us-10-717-984-5.rag

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RESULT 1
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Query Match	Length DB	DB	ID	Description	
1	370	100.0	69	و ا	AAE35863	Aae35863 HMG1 B bo	
7	370	100.0	69	۵	AD025922	Ado25922 High mobi	
٣	370	100.0	69	ω	ADO71481	Ado71481 Human/mou	
4	370	100.0	74	ω	AD025934	Ado25934 High mobi	
v	370	100.0	74	æ	AD071527	Ado71527 Human hig	
φ	370	100.0	74	σ	ADY85362	Human	
7	370	100.0	74	σ	ADY85078	Ady85078 Human HMG	
80	370	100.0	74	σ	ADY85087	Human	
6	370	100.0	75	ω	ADR45941		
10	370	100.0	92	ω	AD025962	2 High m	
11	370	100.0	92	۵	ADO71534 .	-	
12	370	100.0	92	σ	ADY85368	Human	
13	370	100.0	92	σ	ADY85084	Human	
14	370	100.0	128	m	AAB57179	Aab57179 Human pro	
15	370	100.0	168	œ	ABM81641	Abm81641 Tumour-as	
16	370	100.0	176	9	ADA55380	Ada55380 Human pro	
17	370	100.0	214	7	ADD47645	Add47645 Human Pro	
18	370	100.0	214	7	ADE60730	Ade60730 Rat Prote	
19	370	100.0	214	7	ADE60447	Ade60447 Human Pro	
20	370	100.0	214	7	ADES 7980	Ade57980 Human Pro	
21	370	100.0	214	7	ADE57984	Ade57984 Human Pro	
22	370	100.0	214	7	ADE57978	Ade57978 Rat Prote	
23	370	100.0	214	7	ADE60732	Ade60732 Human Pro	
24	370	100.0	214	7	ADE57982	Ade57982 Rat Prote	

Disclosure; Fig 12E; 82pp; English.

Ade60726 Rat Prote Ade60728 Human Pro Ade6045 Rat Prote	Addinan Addinano aci Abb57220 Mouse isc Abu07499 Protein d Aae35859 Human HMG Aae35860 Mouse and Add40789 Human HMG		
ADE60726 ADE60728 ADE60445	AUS17580 ABB57220 ABU07499 AAE35859 AAE35860 ADD40789	ADD40788 ADD47643 ABM85677 ADO60491 ADO25919 ADO25918	ADO71478 ADO71477 ADR45922 ADR87104 ABM81508 ADW81011
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ALIGNMENTS

69 AA

New isolated polypeptide having a vertebrate HWG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes. Rat; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis, hepatitis; appendicitis; peptic ulcer; duodenal ulcer; crohn's disease; meningitis; allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene therapy; human immunodeficiency virus; mouse; human; HMGBI protein. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO) GEN HOSPITAL CORP. (UYPI-) UNIV PITISBURGH. MP; Fink Tracey KJ, Yang H, Warren HS, 15-MAY-2002; 2002WO-US015329. 15-MAY-2001; 2001US-0291034P. AAE35863 standard; protein; entry) WPI; 2003-120594/11. (first WO200292004-A2. Mus sp. Rattus sp. Homo sapiens. 21-NOV-2002. 17-JUN-2003 HMG1 B box AAE35863;

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C. The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-actuaring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by convention of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendictis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, amochiatis, emphysema, HIV infection, candidiasis, malaria, filariasis, amochiatis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, moniptitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is HMGI (also termed as HMGBI) B box found in human, mouse and rat
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1es 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69 AA;
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69 EKYEKDIAA 69 EKYEKDIAA 61 유 ò 셤

RESULT

AD025922 standard; protein; 69 AA. AD025922;

(first entry) 26-AUG-2004

cytostatic; gene therapy; vaccine; pharmaceutical composition; HMGB B box, high mobility group; immune response; immunostimulation; cancer; human; mouse; rat; high mobility group box 1; HMG1; cytokine activity; B box. High mobility group box 1 (HMG1) B box protein sequence.

Mammalia

WO2004046338-A2

03-JUN-2004

19-NOV-2003; 2003WO-US036975

(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. 20-NOV-2002; 2002US-0427848P.

Tracey KJ;

WPI; 2004-420625/39.

New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.

New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.

SEQ ID NO 5; 113pp; English.

Claim 32;

The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that

Disclosure; SEQ ID NO 5; 68pp; English.

The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide CCCCXSXLLLXBXBXBXBXBXBXXBXXBXXBXBXBXCCCCCXSXCCCCCX

ö Human, mouse, high mobility group box 1 B box; HMGB1 B box, HMGB, thMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammation; vertex allograft rejection; rheumation; inflammation; upper adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; chronic, myocardial ischaemia; organic ischaemia; repartusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia; rat. immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human/mouse/rat high mobility group box 1 (HMG1) B box protein sequence that can be used to stimulate cytokine activity and increase immune response to assist in treating disease. 9 9 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK Gaps comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of .; 0 Human/mouse/rat high mobility group box 1 (HMGB1) B box protein. Length 69; Indels ; Score 370; DB 8; ; Pred. No. 3.7e-38; 0; Mismatches 0; Ź (CRIT-) CRITICAL THERAPEUTICS INC. ADO71481 standard; protein; 69 100.08; 100.0%; 20-NOV-2002; 2002US-0427841P. 20-NOV-2002; 2002US-0427846P. 20-NOV-2003; 2003WO-US037507 (first entry) Query Match
Best Local Similarity 100.
Matches 69; Conservative O'keefe TL; EKYEKDIAA 69 EKYEKDIAA 69 WPI; 2004-420628/39. WO2004046345-A2. Sequence 69 AA; Homo sapiens. 26-AUG-2004 03-JUN-2004 Newman W, Rattus sp. 61 ADO71481; Mus sp RESULT 3 ADO71481 88888888888 셤 8 ठ

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specifically bind to the HWGB B box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammentory cytokine from a cell treated with HMGB, a method for effecting weight loops or treating obseity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obseity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obseity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepais, allograft rejection, rheumatoid arthritis, asthma, luques, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion peritonitis, multiple sclaresis or cachexia. This sequence ulcarative a human/mouse/rat HMGBI B box polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 370; DB 8; 100.0%; Pred. No. 3.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 17; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO25934 standard; peptide; 74 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69 AA;
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinfiammarory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) B box biologically active fragment.
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                                                                                                                                                                                                                                                                                                                                               1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammation; cytokine cascade; sepsits; allograft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress synd chronic obstructive pulmonary disease; psoriasis; pancreatitis; perilonitis; burn; myocardial ischaemia; organic ischaemia; schaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
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                                                                                                                                                                                                                                                                  DB 8; Length 74;
                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human high mobility group box (HMGB) B box protein #1.
                                                                                                                                                                                                                                                                ; Score 370; DB 8;
; Pred. No. 4e-38;
0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO71527 standard; protein; 74 AA.
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20-NOV-2002; 2002US-0427846P.
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                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newman W, O'keefe TL;
                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
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Best Local Similarity
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                                                                                                                                                                                                                            Sequence 74 AA;
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Disclosure; SEQ ID NO 37; 57pp; English

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ceffecting weight loss or treating obesity in a patient, a method for effecting weight loss or treating obesity in a patient, a method of detecting weight loss or treating obesity in a patient, a method of detecting whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TNF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease psoriasis, pancreatitis, chronic obstructive pulmonary disease psoriasis, pancreatitis, chronic obstructive pulmonary disease, psoriasis, can including burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB B box polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKOPYEKKAAKLK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
   epitopes of HMGB, where the antibodies can inhibit release of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 370; DB 8; Length 74; I Similarity 100.0%; Pred. No. 4e-38; 69; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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High mobility group box; HMGB1; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiuloer; gastrointestinal-gen.; Crobns disease; inflammation; asthma; antiasthmatic; psoriasis; rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer Human high mobility group box protein HMGB1 B box. ADY85362 standard; protein; 74 AA. (first entry) 02-JUN-2005 ADY85362; ADY85362
XX
AC
ADY
XX
AC
ADY
XX
ADY
XX
High
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KW
High
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KW
CUC|C
XW
CUC|C

WO2005025604-A2. Homo sapiens 24-MAR-2005.

(GEHO) GEN HOSPITAL CORP. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

.0-SEP-2004; 2004WO-US029540. 10-SEP-2003; 2003US-0502349P.

Warren HS, Tracey KJ;

WPI; 2005-233421/24.

Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its immunosuppressive fragment.

The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-ratural HMGB A box. The immune cell fragment of the vertebrate or non-ratural HMGB A box. The immune action into the pathology is induced by the administration of a non-human antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, by the transplantation of an organ into the individual, by the transplantation of an organ into the individual or by infection from a microorganism. Claimed methods of protecting a subject against an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering a HMGB A box, a non-naturally-occurring HMGB A box.

Comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A conditional antigential an autoimmune disorder in an individual comprises administering an HMGB polypeptide comprising a vertebrate and a vertebrate or non-naturally-occurring HMGB box. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, sequence is that of the B box of human HMGBI protein ADY85326. ö 9 64 S NAPKRPPSAPFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK Gaps ; 0 ; Score 370; DB 9; Length 74; ; Pred. No. 4e-38; 0; Mismatches 0; Indels 100.0%; Query Match
Best Local Similarity 100.
Matches 69; Conservative 61 EKYEKDIAA 69 EKYEKDIAA 73 Sequence 74 AA; 셤 ò d ò

ADY85078 standard; protein; 74 AA. 16-JUN-2005 (first entry) Human HMGB1 A box. ADY85078; RESULT 7 ADY85078

sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; periconitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder. High mobility group box; HMGB1; monoclonal antibody; antibody therapy

Homo sapiens Rattus sp. ds sny

WO2005026209-A2.

24-MAR-2005

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Homo sapiens
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                                                                                                                                                                                                                                                    The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated by activation of a proinflammatory cytokine from a vertebrate cell treated by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, postabis, pancreatitis, peritonitis, burns, ischemia, Behnet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus, and identical sequence is that of the A box of human HMGB1. An identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDXQPYEKKAAKLK 64
                                                                                                                                                 New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis; antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiarthmatic; lupus erythematosus; antiainflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 370; DB 9; Length 74; 100.0%; Pred. No. 4e-38; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2; 123pp; English.
                                                                                          Okeefe T, Obar R;
                                                            (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY85087 standard; protein; 74 AA
                              11-SEP-2003; 2003US-0502568P.
10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                   for treating, e.g. sepsis.
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                                                                                                                    WPI; 2005-233483/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                          Qin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 74 AA;
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                                                                                          Newman W,
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The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of control of an inflammatory cytokine cascade, and methods of control of control of an inflammatory cytokine cascade, and inhibits release of conditionally bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HWGB corporation. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, infilammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus, and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1 ADY85012. An identical
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proinflammatory cytokine from a cell treated with HMGB protein, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody or its antigen-binding fragment specific to a vertebrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Obar R;
                                                                                                                                                                                                                                                                                                                              (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR45941 standard; protein; 75 AA.
                                                                                                                                                                                              10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                                                                                                                                                                                                               Okeefe T,
                                                                                                                                                                                                                                                               11-SEP-2003; 2003US-0502568P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating, e.g. sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-233483/24.
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Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   Oin S,
                                                              WO2005026209-A2
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                                                                                                                               24-MAR-2005
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                   Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR45941;
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The present invention relates to the use, especially in vitro, of nucleic acids encoding high mobility group proteins for the following processes: a magingenesis (including in a wound bed), neovascularization, transmyocardial revascularization, wound healing, epithelialization and healing in cases of tooth or bone implants. The sequences and their encoded protein are useful for treating a very wide range of diseases: (proliferation, athritis, endometriosis, histocytosis, psoriasis, rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma, Kaposi sarcoma and basal cell carcinoma), haemorrhoids, atteriosclarosis, angina pectoria, ischaemia, infarction, infertility, wounds (including diabetic and other ulcers), also diseases associated with DNA damage, especially xeroderma pigmentosum, leather skin', skin cancers and ageing cosmetic treatment, especially as a sun-protection composition. Compounds cosmetic treatment, especially as a sun-protection composition. Compounds the protein and all the specified processes can also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutically. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     translation or transcription products, for treating diseases associated with e.g. angiogenesis, neovascularization or wound healing, also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKOPYEKKAAKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Use of nucleic acids encoding basic DNA-binding proteins, and their
cardiant; vulnerary; antiulcer; high mobility group protein; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 370; DB 8; Length 75; l Similarity 100.0%; Pred. No. 4.1e-38; 69; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 57; SEQ ID NO 26; 161pp; German.
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                                                                                                                                                                                              07-MAR-2003; 2003DB-01010160.
10-AUG-2003; 2003DB-01036642.
08-OCT-2003; 2003DB-01046614.
                                                                                                                                             05-JAN-2004; 2004WO-EP000030
                                                                                                                                                                                   2003DE-01000023
                                                                                                                                                                                                                                                                         (ALCE-) ALCEDO BIOTECH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                              WPI; 2004-571355/55.
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Matches 69; Conserv
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                                                                        NO2004061456-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
                                                                                                                                                                                                                                                                                                          Bullerdiek J;
                                         Homo sapiens
                                                                                                                                                                                 03-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2004
                                                                                                            22-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Bahcet's disease; graft-versus-host disease; crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. The composition individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box I (HMGI) B box biologically active fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human high mobility group box (HMGB) B box protein #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 370; DB 8;
100.0%; Pred. No. 5.1e-38;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                       (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 45; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO71534 standard; protein, 92 AA.
                                                                                                                                                                            19-NOV-2003; 2003WO-US036975.
                                                                                                                                                                                                                  20-NOV-2002; 2002US-0427848P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Les 69; Conservative
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                                                                                                                                                                                                                                                                                                                                  WPI; 2004-420625/39.
                                                                                                 WO2004046338-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92 AA;
                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004
                                                                                                                                       03-JUN-2004
                                                                                                                                                                                                                                                                                             Tracey KJ;
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The invention is based on the discovery that high mobility group box canning that a matigen, diminishes the antibody response to the administered antigen. HWGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HWGB polypeptide comprising a vertebrate HWGB A box, or an immunesuppressive fragment of the vertebrate or non-natural HWGB A box. The immune pathology is induced by the administration of a non-human antigen, non-capthology is induced by the administration of a non-human antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering a HWGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box. A claimed method of treating an auto-maturally-occurring HWGB A comprises administering a HWGB polypeptide comprising a vertebrate HWGB A box, or an immunosuppressive fragment of these, and a vertebrate or non-naturally-occurring HWGB B box, and naminosuppressive fragment of these, and a vertebrate or non-naturally-occurring HWGB C box, and may allease is alleady, and a vertebrate or non-naturally-occurring HWGB C box, and mind may be a preferably a HWGBI peptide and may be considered at the C-terminus. The autoimmune disease is alleady, and a vertebrate or non-naturally-occurring HWGB become and may be an antifered at the C-terminus. The unifered and may be an antifered at the C-terminus. The unifered and may be an antifered at the C-terminus. The unifered at the C-terminus and a vertebrate or non-naturally-occurring HWGB perminus and a vertebrate or non-naturally-occurring and a vertebrate or non-naturally-occurring and a vertebrate or non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
ulcerative colitis, antiinflammatory; antiulcer; gastrointestinal-gen.; Crohna disease; inflammation; asthma; antiashmatic; rheumatoid arthritis; antitheumatic; antiathritit; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis or systemic lupus erythematosus (all claimed). The present sequence is that of the B box of human HMGB1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 370; DB 9; Length 92; larity 100.0%; Pred. No. 5.1e-38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP.
(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 43; 57pp; English.
                                                                                                                                                                                                                                                                         10-SEP-2004; 2004WO-US029540.
                                                                                                                                                                                                                                                                                                                      10-SEP-2003; 2003US-0502349P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tracey KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-233421/24.
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKYEKDIAA
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                                                                                                                                                                        WO2005025604-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 92 AA;
                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                        24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                              Warren HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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ADY85084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammentory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B conceptionally bind to the HMGB B box but do not specifically bind to non-B conceptionally where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the patient comprises administering composition and methods are useful in treating obesity and conditions characterised by activation of an useful in treating obesity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                           New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, rheumatory cytokine cascade, e.g. sepsis, allograft rejection, chromatod arthritis, asthma, lugus, adult respiratory distress syndrome, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcer's disease, graft-vereus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB B box polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 370; DB 8;
100.0%; Pred. No. 5.1e-38;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 58; 113pp; English.
                                                                                                                                                                                                                                             (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADY85368 standard; protein; 92 AA.
                                                                                                                       20-NOV-2003; 2003WO-US037507.
                                                                                                                                                                     20-NOV-2002; 2002US-0427841P.
20-NOV-2002; 2002US-0427846P.
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                                                                                                                                                                                                                                                                                             O'keefe TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-420628/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                            WO2004046345-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                                Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Gaps

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New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful High mobility group box; HMGB1; monoclonal antibody; antibody therapy; sepsis; antibacterial immunosupressive; graft rejection; arthritis; antiatrhritic; asthma; antiasthmatic; lupus erythematosus; antiasthmatic; lupus erythematosus; antiaflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; asstrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder. Disclosure; SEQ ID NO 2; 123pp; English Obar R; (CRIT-) CRITICAL THERAPEUTICS INC. ADY85084 standard; protein; 92 AA Okeefe T, 10-SEP-2004; 2004WO-US029527 11-SEP-2003; 2003US-0502568P for treating, e.g. sepsis. (first entry) WPI; 2005-233483/24. Qin S, Human HMGB1 A box WO2005026209-A2 Homo sapiens 16-JUN-2005 24-MAR-2005 Mus sp. Rattus sp. Newman W,

The invention provides antibodies, or their antigen-binding fragments, that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB A box but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB protein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, penitonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, arthritis, arthritise, present sequence is that of the A box of human HMGB1. An identical sequence is also found in rat and mouse HMGB1.

Sequence 92 AA;

ö 9 NAPKRPPSAFFLFCSEYRPKI KGEHPGLSI GDVAKKLGEMMNNTAADDKQPYEKKAAKLIK NAPKRPPSAFFLFCSEYRPKI KGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK Gaps ö Length 92; 0; Indels 100.0%; Score 370; DB 9; 100.0%; Pred. No. 5.1e-38; iive 0; Mismatches 0; Local Similarity 100. Query Match Matches

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69 73 EKYEKDIAA EKYEKDIAA 61 셤 à

AAB57179 RESULT

AAB57179 standard; protein; 128 AA.

13-MAR-2001 (first entry)

Human prostate cancer antigen protein sequence SEQ ID NO:1757.

Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.

Homo sapiens.

WO200055174-A1.

21-SEP-2000

08-MAR-2000; 2000WO-US005988

99US-0124270P 12-MAR-1999;

(HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.

Rosen CA, Ruben SM;

2000-587513/55.

N-PSDB; AAF16382

Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer

Claim 11; Page 2225-2226; 2338pp; English

proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunoamodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and prolliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present AAF15566 to AAF16505 encode the human prostate cancer associated

Sequence 128 AA;

; 0 Length 128; Indels Query Match 100.0%; Score 370; DB 3; Best Local Similarity 100.0%; Pred. No. 7.6e-38; Matches 69; Conservative 0; Mismatches 0;

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61 EKYEKDIAA 69

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|||||||||||||| EKYEKDIAA 78

RESULT 15

ABM8164

ABM81641 standard; protein; 168 AA.

ABM81641;

(first entry) 18-NOV-2004

Tumour-associated antigenic target (TAT) polypeptide PRO82460, SEQ:4238.

Tumour-associated antigenic target, TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.

Homo sapiens

WO2004030615-A2

15-APR-2004.

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(GETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32. N-PSDB; ACN39840 New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12; SEQ ID NO 4238; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide and polypeptides at least 80% identical to the TAT nucleic acids and polypeptides are sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; a peptide or organic acid; an antibodies, antagonists, binding molecules and compositions for the treatment or diagnosing or treating a cell proliferative disorder associated with cincreased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence

Sequence 168 AA;

ö Gaps ö 100.0%; Score 370; DB 8; Length 168; 100.0%; Pred. No. 1e-37; Live 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 69; Conservative

61 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWINTAADDKQPYEKKAAKLK 120 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60 g ò

69 61 EKYEKDIAA

121 EKYEKDIAA 129

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6, 2006, 10:19:12 Search completed: April Job time: 83.7533 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                     Copyright
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OM protein - protein search, using sw model

2006, 10:19:38; Search time 13.1645 Seconds (without alignments) 504.309 Million cell updates/sec 6 9 Run

US-10-717-984-5

1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA 69 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nonhistone chromos	nonhistone chromos	nonhistone chromos	nonhistone chromos	non-histone chromo	nonhistone chromos	nonhistone chromos	high mobility grou	nonhistone chromos	nonhistone chromos	nonhistone chromos	nonhistone chromos	high-mobility grou	ţ	nonhistone chromos	힡	HMG-1 - chicken	nonhistone chromos	high mobility grou	nonhistone chromos	nonhistone chromos		DNA-binding protei	structure-specific	high mobility grou	high mobility grou	protein -	dorsal switch prot	nonhistone chromos
SUMMARIES	ΩI	A27853	NSRTH1	S01947	S02826	148688	A28897	S29857	S62355	S30221	NSHUH2	A34719	JC1129	JC1114	S54774	A24019	S48708	I50254	S22359	T01071	S26062	B61611	151067	A41265	A41976	T03374	878050	JC4357	JC6179	820068
	DB	~	-	-	~	~	7	~	7	~	-	7	~	~	~	~	~	7	7	7	~	~	7		~				N	7
	Length	170	215	215	215	215	215	216	210	186	209	210	207	207	210	172	204	201	202	204	202	186	215	708	709	138	699	200	393	393
de	Query Match	100.0	100.0	100.0	100.0	100.0	98.6	97.3	90.5		87.6	87.6	86.8	86.2	85.4	81.4	81.4	81.1	81.1	80.5	79.5	78.9	71.1		45.9	45.5		44.9	44.9	44.9
	Score	370	370	370	370	370	365	360	335	324	324	324	321	319	316	301	301	300	300	298	294	292	263	172	170	168.5	168	166	166	166
	Result No.	-	7	9	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

probable high mobi	high mobility grou	nonhistone chromos	high mobility grou	mobility	ity	transcription fact	high mobility grou	İty	high mobility grou	high mobility grou	high mobility grou	HMG protein [impor	nonhistone chromos	high mobility grou	high mobility grou
T09581	S35637	A35072	S39556	T03372	T07377	T12113	B47150	S18991	T03640	T02252	S40302	T51159	878076	T03375	T51598
~	~	N	~	~	~	7	~	~	~	7	~	~	7	~	N
141	561	93	149	139	141	642	157	161	168	142	144	178	66	126	141
14.5	44.3	44.1	43.9	43.4	43.1	43.0	42.8	42.8	42.8	42.6	42.6	42.3	42.2	42.0	41.2
٧.			2	'n	'n	159	7	.5	5.5	50	'n	ņ	156	.55.5	s.
164.5	164	163	162.	160.5	159	7	158	158	158	157	157	156.5	7	155	152.5

ALIGNMENTS

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	1	
	HMG-1	
	1 protein HMG-1	
	histone chromosomal protein HMG-1 - C	
ULT 1 853	histone	

C;Species: Cricetulus griseus (Chinese hamster) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004 hinese hamster (fragment)

Ribe, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A; Title: Characterization of cDNA sequences corresponding to three distinct HWG-1 mRNA signification of cDNA sequences corresponding to three distinct HWG-1 mRNA signeference number: A27853, WUID:8725986; PMID:3601666
A,Accession: A27853
A,Molecule type: mRNA
A,Residues: 1-170 <LEE>
A,Residues: 1-170 <LEE>
A,Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C;Superfamily: nonhistone chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>

Gaps ô / Match 100.0%; Score 370; DB 2; Length 170; Local Similarity 100.0%; Pred. No. 3.8e-33; hes 69; Conservative 0; Mismatches 0; Indels Best Loc Matches

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108 EKYEKDIAA 116 61 EKYEKDIAA 69 ò 셤

RESULT

nonhistone chromosomal protein HMG-1 - rat

NyAlternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Dapecies: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A41175; A27298; Ā30188; B48771; A48771; C48771
R;Meremmies, J; Pihlaskari, R; Laitinen, J; Wartiovaara, J; Rauvala, H.
J;Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-KDa heparin-binding protein of brain (amphoterin) involved in neurite outgro
A;Reference number: A41175; MUID:91358468; PMID:1885601

A, Accession: A41175 A, Molecule type: mRNA A, Residues: 1-215 < MER>

A;Cross-references: UNIPROT:P07155; UNIPARC:UPI0000008A6; GB:M64986; NID:g202884; PIDN:. A;Note: part of this sequence, including the amino end of the mature protein, was confir. A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in

h-mobility group proteins R;Paonessa, G.; Frank, R.; Cortese, R. Nucleic Acids Res. 15, 9077, 1987

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Gaps

9

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A; Molecule type: protein
A; Mesidues: 2-22, 7x, 24.38 cCHR>
A; Cross-references uniparc: UP10000173989
A; Cross-references uniparc: UP10000173989
B; Dentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A; Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group, A; Reference number: 145910, MUID:84128872; PMID:6141822
A; Accession: 145910
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mANA
A; Mol
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A;Molecule type: mRNA
A;Cross.references: UNIPROT:P09429; UNIPARC:UPI00000115ED; EMBL:X12597; NID:g32326; PIDN
R;Mard, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma proti
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C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: 802826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Avclaic Acida Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: 802826; MUID:89160247; PMID:2922262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 152
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C,Superfamily: nonlistone chromosomal protein HMG-2; HMG box homology
C,Keywords: chromosomal protein; DNA binding; nucleus
F,6-83/Domain: HMG box homology <HMG1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nonhistone chromosomal protein HMG-1 - human
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A;Molecule type: protein
A;Residues: 2-13,'XXF' <WAR>
A;Cross-references: UNIPARC:UP100001771D7
A;Accession: G33178
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A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UP100001771D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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Matches 69; Conservative 0.
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A;Residues: 2-14, 'X',16-21 <RAU>
A;Residues: 2-14, 'X',16-21 <RAU>
A;Cross-references: UNIPARC:UPI0000173985
R;Parkkinnen, J; Raulo, E; Merenmies, J; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauval J. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMC1-type polypeptides. Enhanced A;Reference number: A48771; MUID:93374971; PMID:8366113
A; Title: Nucleotide sequence of rat liver HWG1 cDNA.
A; Reference number: A27298; MUID:88067717; PMID:3684582
A; Accession: A27298
A; Accession: A27298
A; A; Accession: A27298
A; A; Conserved: WIPARC:UPID:0000173984
A; Cross-references: UNIPARC:UPID:0000173984
B; Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P. J. Cell Biol. 107, 2293-2305, 1988
A; Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
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A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
A,Rocession: A61611
A,Molecule type: protein
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
B;Cross-references: UNIPARC:UPD10000173987; UNIPARC:UPD1000173988
B;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
A;Reference number: S10726; MUID:90306387; PMID:2365081

A;Reference number: S10726; MUID:90306387; PMID:2365081
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$01947
nonhistone chromosomal protein HMG-1 - bovine
N.Alternate names: 33K protein, high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S01947, Aci611; S10859; 145910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res: 16, 10375, 1989
A;Attle: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUD:89057489; PMID:3194213
A;Accession: S01947
A;Residues: 1-215 <KAPP.
A;Residues: 1-215 <KAPP.
A;Residues: 1-215 <KAPP.
A;Accession: A;Accession: A;Alta A;Alta A;Alta A;Alta A;Alta A;Accession: A;Alta A;A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A30188; MUID:89066894; PMID:2461949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 370; DB 1; 100.0%; Pred. No. 4.9e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conservative
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A;Cross-references: UNIPARC:UP1000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI A;Note: the authors did not translate the codon for residue 1 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein C;Keywords: chromosomal protein F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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A;Note: the authors did not translate the codon for residue 1
A;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>
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Rividhtingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
A; Title: Evidence for a shared structural role for HMG1 and linker histones B4 and A; Reference number: S62355; MUID:96174815; PMID:8599938
A; Accession: S62355
                                                                                                                                                                                                                                                                                                     93 NAPKRLPSAPFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKKL 152
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C;Dacte: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29857
R;Stros, M.; Dixon, G.H.
Biochim. Bajophys. Acta 1172, 231-235, 1993
A;Title: A retropseadogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                      1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DMA binding; nucleus F;6-83/Domain: HMG box homology cHMG1> F;92-166/Domain: HMG box homology cHMG2>
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                                                                                                                                                 98.6%; Score 365; DB 2;
98.6%; Pred. No. 1.7e-32;
live 0; Mismatches 1
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les 68; Conservative
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153 EKYEKDIAA 161
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A; Status: preliminary
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148688
non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148689; A55402; T57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nuclectide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc
A;Reference number: 148687; MUID:92335012; PMID:1630928
A;Accession: 148688
A;Accession: 148688
A;Reference number: AREA
A;Molecule type: mRNA
A;References: UNIPROT:P07155; UNIPARC:UP100000008A6; EMBL:Z11997; NID:g53381; PIDN
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J; Biol. Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402
A;Crossion: A55402
A;Status: preliminary; not compared with conceptual translation
A;Rolecule type: DNA
A;Residues: 1-189, E', 191-215 FEREA
A;Residues: 1-189, E', 191-215 FEREA
A;Residues: 1-189, E', 191-215 FEREA
A;Crossereferences: UNIPARC:UP1000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C. M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm: Genome 5, 91-99, 1994
A;Title: Malagle, D.L.; Bucan, M.; Lo, C.W.
Mamm: Genome 5, 91-99, 1994
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C;Genetics:
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Dacesion: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HWG1 revealed by the nucleotide in A;Title: Primary structure of non-histone protein HWG1 revealed by the nucleotide in A;Nolecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: TSU>
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A;Reference number: 157021; MUID:94235965; PMID:9180479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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100.0%; Pred. No. 4.9e-33;
iive 0; Mismatches 0;
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-215 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: nonhistone chromosomal pro
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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                                                                   FKYEKDIAA 161
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                                 69
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                                 EKYEKDIAA
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Best Local Similarity
                                 19
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C; Accession: A34719
R; Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemiatry 29, 4419-4423, 1990
A; Title: Primary 29, 4419-4423, 1990
A; Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucleon A; Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucleon A; Reference number: A34719, MUID: 90275208; PMID: 2350545
A; Accession: A34719
A; Status: preliminary
A; Status: preliminary
A; Status: 1-210 <SHI>A; A; Cross-references: UNIPROT: P17741; UNIPARC: UP1000016C6C5; GB: 302895; NID: 9164491; PIDN: P; Reywords: chromosomal protein; DNA binding; nucleus
F; 6-83/Domain: HMG box homology <HMG1>
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C.Species: Gallus gallus (chicken)
R.Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A.Fitle: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Fitle: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Fitle: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Fitle: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Fitle: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Fitle: Sequence of a cDNA encoding protein HMG-2; HMG box homology
C.Superfamily: nonbistone chromosomal protein; DNA binding; nucleus
F.6-83/Domain: HMG box homology <HMG2>
F.92-166/Domain: HMG box homology <HMG2>
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C,Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                       1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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                                       C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: chromosomal protein; DMA binding; nucleus F;6-83/Domain: HMG box homology <HMG1> F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                            Length 209,
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87.0%; Pred. No. 5.1e-28;
tive 4; Mismatches 5;
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                        Score 324; DB 1,
Pred. No. 5e-28;
4; Mismatches

    chicken

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Best Local Similarity 87.0%;
Matches 60; Conservative
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   A; Map position: 7pter-7qter
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153 EKYEKDIAA 161
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JC1129
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NSHUH2

nonhistore chromosomal protein HMG-2 - human
C)Species: Homo sapiens (man)
C,Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
C,Accession: A42425, S20061; $18068
R;Ahcession: A42425, S20061; $18068
R;Ahcession: A42425
A,Title: Structure of a gene coding for human HMG2 protein.
A,Feferance number: A42425, MUID:92202209; PMID:1551873
A,Recession: A42425
A,Molecule type: DNA
A,Residues: 2-209 <AHr
A,Residues: 2-209 <AHr
A,Residues: 2-209 <AHr
A,Residues: DNA
A,Residues: DNA
A,Residues: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:9184235; PIDN:
A,Rocession: A2426
A,Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A,Note: initiator Met not shown
R,Msjundar, A.; Brown
D, Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643, 1391
A,Title: Sequence of human HMG2 cDNA
A,Residues: 220061; MUID:92093633; PMID:1754403
A,Recession: S20061
A,Molecule type: mRNA
A,Residues: 1-209 <AMAA.
A,Residues: L-209 <AMAA.
A,Residues: L-200 <AMAA
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October 1992
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C;Genetics:
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                                                                                                                                               70 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEGSAKDKQPYEQKAAKLK 129
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: UNIPROT: P26583; UNIPARC: UPI000016AA6C; EMBL: Z17240; NID: 93
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, Octobe C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology (; Keywords: chromosomal protein F: 1-60/Domain: HMG box homology (fragment) < HMG>
F: 1-60/Domain: HMG box homology (HMG1>
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S30.21
C;Accession: S30.21
Nucleic Acids Res. 20, 6413, 1992
A;Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A;Reference number: S30221; MUD:93117123; PMID:1475204
                                                                                                       1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK
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                                          Gaps
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Pred. No. 4.4e-28;
4; Mismatches 5; Indels
   85.5%; Pred. No. 3.2e-29;
iive 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
S30221
nonhistone chromosomal protein HMG-2B - human (fragment)
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A,Cross-references: GDB:119451; OMIM:118880
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Best Local Similarity 87.0%;
Matches 60; Conservative
                                   59; Conservative
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EKYEKDVAA 160
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Best Local Similarity
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NiAlternate names: HMG-T
C;Species: Salmo sp. (trout)
Cjate: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24019
R;Pentecoat, B.T.; Wright, J.M.; Dixon, G.H.
R;Pentecoat, B.T.; Wright, J.M.; Dixon, G.H.
Avcleic Acida Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NAPKRPSSAFFIFCADFRPQVKGETPGLSIGDVAKKLGEKMNNLTAEDKVPYEKKASKLK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P07746; UNIPARC:UP100001771D6
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: Chromosomal protein; DNA binding; nucleus
F;1-50/Domain: HMG box homology (fragment) <HMG1>
F;59-133/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
81.4%; Score 301; DB 2; Length 172;
Best Local Similarity 78.3%; Pred. No. 1.3e-25;
Matches 54; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                 nonhistone chromosomal protein HMG-T - trout (fragment)
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153 EKYEKDIAA 161
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A;Molecule type: mRNA
A;Residues: 1-172 <PEN>
                                                                                                                                                        A24019
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                                                                                                                                                                                                                                                                                                                                                                                                     high-mobility group protein 2 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: O9-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C; Accession: JC1114
R; Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A; Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt A; Reference number: JC1114; MUID:92241676; PMID:1572546
A; Accession: JC1114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: UNIPROT:P26584; UNIPARC:UP10000171347; GB:M83235; NID:g211926; PIDN: C;Comment: The high mobility group proteins are among the most abundant nonhistone chrom C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology C;Keywords: DNA binding; nucleus P;6-83/Domain: HMG box homology <HMG1> P;92-166/Domain: HMG box homology <HMG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S5221
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Ttle: High mobility group protein 2 functionally interacts with the POU domains of A;Reference number: S54774; MUID:95237201; PMID:7720710
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86.2%; Score 319; DB 2; Length 207;
Best Local Similarity 85.5%; Pred. No. 1.8e-27;
Matches 59; Conservative 4; Mismatches 6; Indels
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85.5%; Pred. No. 1.1e-27;
tive 5; Mismatches 5;
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                                  59; Conservative
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Best Local Similarity
Matches 59; Conserv
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A; Residues: 1-207 < DAV>
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GenCore version 5.1.7
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April Run on:

6, 2006, 10:13:48; Search time 81.4836 Seconds (without alignments) 597.439 Million cell updates/sec

US-10-717-984-5 370 1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA 69

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O8c7c4 mus musculu	P07156 cricetulus	Q8bnm0 mus musculu	Q5t7c5 homo sapien	P10103 bos taurus	Q6yka4 canis famil	P09429 homo sapien	mus m	P63159 rattus norv	Q5t7c3 homo sapien						rattus	m high	gallus	gallus	BUB B	homo	เพนย แ	Q8bq02 mus musculu	mus m	homo	homo	homo	homo	homo	xenor	Q7sz42 xenopus lae
αI	Q8C7C4 MOUSE	HMG1 CRIGR	Q8BNMO MOUSE	10	HMG1 BOVIN	HMG1_CANFA	HMG1 HUMAN	HMG1_MOUSE	HMG1 RAT	Q5T7C3_HUMAN	Q4R844 MACFA		O88612_SPAEH		Q9QX40_SPAEH	Q548R9_RAT	QS8EVS_MOUSE	Q9PUK9_CHICK	Q9YH06_CHICK	HMG1_PIG		Q6P202_MOUSE	Q8BQ02_MOUSE	Q5BKQ1 MOUSE	HMG1X HUMAN		Q5T7C2 HUMAN	Q5T7C4_HUMAN	Q59GW1 HUMAN	Q6P4N5_XENTR	Q7SZ42_XENLA
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.9	98.9	98.6	98.6	98.4	97.3	97.0				95.1	95.1		91.1
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Q91596 xenopus lae Q6gng5 xenopus lae	Q96j53 homo sapien P26583 homo sapien Q5u071 homo sapien	P17741 sus scrofa P52925 rattus norv O5u072 homo sapien	Q5fvp0 rattus norv Q9n1q5 hylobates 1 Q8ch24 mus musculu	Q6y235 pagrus majo P26584 gallus gall O9n107 pan troglod	4
2 Q91596_XENLA 2 Q6GNQ5_XENLA	2 Q96JS3_HUMAN 1 HMG2_HUMAN 2 Q5U071_HUMAN	HMG2_PIG HMG2_RAT O5U072_HUMAN	OSFVPO_RAT SP100 HYLLA OBCH24 MOUSE	Q6Y235_PAGMA HMG2 CHICK SP100 PANTR	1
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R. EMBL, AKOSOGS9, BACJ4J67.1; -; mRNA.
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                                                                                                                                           Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wubtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Nagada K., Nagada K., Nagada K., Nagada K., Nagada M., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mataminoto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawi T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika I., Matamatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rishika I., Matsuira B., Matsuira B., Matamatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rishi M., Ishika I., Matamatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rishi M., Ishika M., 
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MGI; MGI:9613; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005634; F:intric-oxide synthase regulator activity; IDA.

GO; GO:0006809; F:intric-oxide biosynthesis; IDA.

GO; GO:0006809; P:intric-oxide biosynthesis; IDA.

GO; GO:0006810; P:ransport; IDA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000191; HMG_12_box.
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                                                                                     STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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100.0%; Pred. No. 1.4e-31;
ive 0; Mismatches 0;
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SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
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Nature 420:563-573(2002)
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PRINTS; PR00886; HIGHMOI
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RESULT 🏖

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GO: 0000191; P:DNA bending activity; ISS.
GO: 000011; F:DNA bending activity; ISS.
GO: GO: 0000518; F:protein binding; ISS.
GO: GO: 0000528; P:base-excision repair, DNA ligation; ISS.
GO: GO: 0000528; P:DNA recombination; ISS.
GO: GO: 0000528; P:DNA repair; ISS.
GO: GO: 0000528; P:DNA repair; ISS.
GO: GO: 0000528; P: establishment and/or maintenance of chromat. . .; ISS.
GO: GO: 0017055; P: establishment and/or maintenance of chromat. . .; ISS.
InterPro; IPR00010; HMG 12_box.
FEan; PR00805; HMG box; Z.
FRINTS; PR00806; HIGHMOBLTY12.
                                                01-APR-1988 (Rel. 07, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein B1)
                                                                                                   (Fragment).
Name=HMGB1; Synonyms=HMG-1, HMG1;
Cricetulus griseus (Chinese hamster).
Bukaryota; Metaeo; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metaeo; Chordata; Craniata; Vertebrata; Eutheria; Buarohontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
NCB1_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93347974; PubMed=8346022;
Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
"Solution structure of a DNA-binding domain from HMG1.";
Nucleic Acids Res. 21:3427-3436(1993).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
double stranded DNA.
                                                                                                                                                                                                                                                                                                             "Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle expression of the HMG-1 gene."; Nucleic Acids Res. 15:5051-5068(1987).
                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=87259986; PubMed=3601666;
Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00353; HWG BOX 1; 1.
PROSITE; PS50118; HWG BOX 2; 2.
3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-1- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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HMG box 2.
Asp/Glu-rich (acidic).
180 AA
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PIR; A27853; A27853.
                                01-APR-1988 (Rel. 07, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB, 1HSM; NNR; @=58-136.
PDB; 1HSN; NNR; @=58-136.
PDB; 1NHM; NNR; @=58-136.
PDB; 1NHN; NNR; @=58-136.
 STANDARD;
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151
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Q5T7C5_HUMAN
       장 ; 원
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                                                                                                                                                                                                                                                58 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKIGEMMNTAADDKQPYEKKAAKKI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body CDNA, RIKEN full-length enriched library, clone:C430013M12 product:high mobility group box 1, full
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The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                       1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murines; Mus.
                                                                                                                                                                          Gaps
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                        Length 180;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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97
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20904 MW; F624392F41609854 CRC64;
                                                                                                                        100.0%; Score 370; DB 1; 100.0%; Pred. No. 1.4e-31;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                        0; Mismatches
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence. (Fragment)
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QBBNMO;
                                                                                                                                                                        69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 118 EKYEKDIAA 126
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                                                                        180 AA;
                                                                                                                     Query Match
Best Local Similarity
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Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Habizume W.,
Pukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hari F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S.,
A Kutihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakazuwe N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (Apr-2002) to the EMBL/Genbank/DDBJ databases.
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                             MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Moranization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Aizawa K., Nagacka S., Sasaki N., Carninci P., Sknho H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Yanamoto R., Matsumnta S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000)
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MGI; MGI:96113; Hmgbl.

MGO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; F:nitric-oxide synthase regulator activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

GO; GO:0006810; P:nitric oxide biosynthesis; IDA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000190; HMG box; Z.

Pfam; PF00505; HMG box; Z.
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Pred. No. 1.4e-31;
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100.0%; Score 370; D
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 69; Conservative 0; Mismatches
STRAIN=C57BL/6J; TISSUE=Whole body;
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PROSITE; PS50118; HMG BOX 2; 2.
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PRINTS; PR00886; HIGHMOBLTY12.
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153 EKYEKDIAA 161
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mobility-group protein (HMG-1).";
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                                                                                                                                                          Pedan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Is bubmitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
R EMBL; AL353648 CAL15602.1; -; Genomic_DNA.
R SNR; QSTYCS; 2-84, 93-171.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005637; F:DMS binding; IEA.
R GO; GO:0005637; F:PROB binding; IEA.
R GO; GO:0005637; F:PROB binding; IEA.
R InterPro; IPR000135; Highmoblty_12.
R InterPro; IPR000139; Highmoblty_12.
R Fam; PR00505; HMG box; 2.
R Fam; PR00505; HMG, 2.
R SNART; SN00398; HMG; 2.
R SNART; SN00398; HMG BOX 1; 1.
R PROSITE; PS00183; HMG BOX 1; 1.
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HWG1_BOVIN STANDARD; PRT; 214 AA.
P10103;
01-MAR-1989 (Rel. 10, Created)
01-MAG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84128872; PubMed=6141822;
Pentecost B., Dixon G.H.;
"Isolation and partial sequence of bovine cDNA clones for the high-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Holstein; TISSUE=Fetal thymus;
BDDINES=89657489; PubMed=3194213;
Kaplan D.J., Duncan C.H.
Replan D.G., Sequence for bovine high mobility group 1 (HMG1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=HMGB1; Synonyms=HMG1;
Bos taurus (Bovine).
Eukaryota: Metazosa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                   192 AA; 22050 MW; 6A52DB61DA307C1D CRC64;
                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment).
Name=HMGB1; ORFNames=RP11-550P23.1-001;
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 370; DB 2;
100.0%; Pred. No. 1.5e-31;
ative 0; Mismatches 0;
 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 16:10375-10375(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA].
QST7CS HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 EKYEKDIAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKYEKDIAA 69
                                                                                  Homo sapiens (Human).
                                                                                                                                         [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                SEOUENCE
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EMBL; X12796; CAA31284.1; -; mRNA.

EMBL; X12796; CAA31284.1; -; mRNA.

EMBL; M26110; AAA30567.1; -; mRNA.

EMBL; M26110; AAA30567.1; -; mRNA.

ENTR; P01103; 1-83, 92-170.

SNR; P10103; 1-83, 92-170.

GO; GO:0006301; F:DNA bending activity; ISS.

GO; GO:0006288; F:Drotein binding; ISS.

GO; GO:0006288; F:DNA recombination; ISS.

GO; GO:0006288; F:DNA repair; ISS.

GO; GO:0006288; F:DNA repair; ISS.

GO; GO:0006288; F:DNA repair; ISS.

GO; GO:0006388; F:DNA unwinding; ISS.

RO; GO:0006388; F:DNA unwinding; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                              MEDLINE-81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4; Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.; "The primary structures of non-histone chromosomal proteins HMG 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6; Christen T., Bischoff M., Hobi R., Kuenzle C.C.; Fish mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not to other types of Z-DNA."; PEBS Lett. 267:139-141(1990).

-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 370; DB 1; Length 214; 100.0%; Pred. No. 1.7e-31; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
Chromosomal protein; Direct protein sequencing; DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C -> S (in Ref. 3).
C -> A (in Ref. 3).
EHPGL -> PGGGV (in Ref. 2).
E -> D (in Ref. 3).
B => B (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
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                                                                              PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMG box 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 HF
214 As
22 C
105 C
119 EF
193 EF
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                                                                                                                                                                                                                                                                            FEBS Lett. 122:264-270(1980).
losci. Rep. 4:49-57(1984)
                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 1-36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 EKYEKDIAA 160
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105
115
193
214 AA;
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:1197-1214(1989)
                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
                                                               B1).
Name=HMGB1; Synonyms=HMG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 35:367-371(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSUE-Small intestine;
                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                 NCBI_TaxID=9606;
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2293580; PubMed-14571134; DOI-10.1159/000073415; Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M., Bullerdiek J., Nolte I.; Bullerdiek J., Nolte I.; Molte I.; Cytogenet Genome Res. 101:33-38(2003).

-! FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA (By similarity).

-! SUBCELLULAR LOCATION: Nuclear (By similarity).

-! SIMILARITY: Belongs to the HMG1/HMG2 protein family.

-! SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                        10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SW00398; HMG; 2.
SROSITE; PS00353; HMG BOX_1; 1.
PROSITE; PS50118; HMG BOX_2; 2.
Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 214 Asp/Glu-rich (acidic).
214 Aa; 24763 MW; B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY135519; AAN11296.1; -; mRNA.
EMBL; AY135521; AAN1319.1; -; Genomic_DNA.
HSSP; PO7155; 1AAB.
RX; OGYKA4; 1-83, 92-170.
ENSEMBL; ENSCAFG0000006597; Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
HMG box 1.
HMG box 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA.
                                                                                   214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12 box.
Pfan; PF00505; HMG box; 2.
PRINTS; PR00886; HĪGHMOBLTY12.
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P09429; Q61BE1;
01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Conservative
                                                                                STANDARD;
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152 EKYEKDIAA 160
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                 Name=HMGB1;
                                                                                   CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT MET
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Q6YKĀ4;
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                                  RESULT 6
HMG1 CANFA
DT HMG1 CANFA
DT 10-MAY.
DT 10-MAY.
DT 10-MAY.
DT 10-MAY.
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CO E BURBLY
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HMG1 HUMAN
ID HMG1 H1
AC P09429
DT 01-MAR
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Matches

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TISSUE-Brain, Cervix, and Testis factor.

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RETAUSDERG R.L., Zeeberg B., Bencow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Districtenco L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Louchman J.W., Gaere E.D., Dickson M.C.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Garimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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"Cloning of human full open reading frames in Gateway(TM) system entry
vector (pDONR201).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A., "Cloning of human full-length CDSs in BD Creator(TM) system donor
01-AUG-1990 (Rel. 15, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=89160247; PubMed=2922262;
Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
"A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96299787; PubMed-8661151; DOI=10.1006/geno.1996.0369; Ferrari S., Finelli P., Rocchi M., Bianchi M.E.; "The active gene that encodes human high mobility group 1 protein (HMG1) contains introns and maps to chromosome 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The German cDNA consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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NUCLEOTIDE
                                                                                                                    HMG1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..., TAS.
.., IDA.
        ; 163905; -. Geondensed chromosome; IDA.
GO:00007931; F:DNA bending activity; TAS.
GO:0008134; F:transcription factor binding; TAS.
GO:0006218; P:Dase-exclsion repair, DNA ligation; IDA.
GO:0006281; P:DNA recombination; TAS.
GO:0006281; P:DNA repair; TAS.
GO:0006288; P:DNA unwinding; NAS.
GO:0006225; P:establishment and/or maintenance of chromat.
GO:0017055; P:negaliation of transcriptional prei.
GO:0006357; P:regulation of transcriptional prei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000135; Highmoblty_12.
Pfam, PF00505; HMG box, 2.
SMART; SM00396; HMG box, 2.
SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 1; 1.
Chromosomal protein; Direct protein sequencing; DNA-binding;
                                                                                                                                                 P04637:TP53; NDExp=1; IntAct=EBI-389432, EBI-386083; O15350:TP73; NDExp=1; IntAct=EBI-389432, EBI-389606; -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-1- SIMILARITY: Contains 2 HMG box DNA-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asp/Glu-rich (acidic).
E -> D (in Ref. 5).
B3C6A80FC7F0F433 CRC64;
                                                                                                                                                                                                                                                                                                                  EMBL, X12597; CAA31110.1; -; mRNA.
EMBL, U31677; AAB08987.1; -; Genomic_DNA.
EMBL, AY377859; AAQ91389.1; -; mRNA.
EMBL, CR749614; CAH18408.1; -; mRNA.
EMBL, ENG6863; CAG33144.1; -; mRNA.
EMBL, BT006940; AAB35866.1; -; mRNA.
EMBL, BC003378; AAV33961.1; -; mRNA.
EMBL, BC003378; AAH03378.1; -; mRNA.
EMBL, BC06889; AAH6389.1; -; mRNA.
EMBL, BC066889; AAH66889.1; -; mRNA.
EMBL, BC066889; AAH66889.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSG0000189403; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, S02826; S02826.
HSSP; P07156; 1NHN.
SMR; P09429; 1-83, 92-170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC; HGNC: 4983; HMGB1.
H-InvDB; HIX0011209; -.
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GO; GO:0008301
GO; GO:00083134
GO; GO:0006288
GO; GO:0006281
GO; GO:000628
GO; GO:0006268
GO; GO:0006268
GO; GO:0006268
GO; GO:0006268
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CONFLICT
SEQUENCE
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Gaps

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1; Length 214; 31; 0; Indels

100.0%; Score 370; DB 1; 100.0%; Pred. No. 1.7e-31;

0; Mismatches

69; Conservative

Matches

Similarity

Query Match Best Local 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 60

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RAY MULLILLE SUCURING LUANCES CLAULE FROMEN IN WINDLILLE SUCURING LUANCES CLAUS CRANGE IN MACHINE 12388257; PubbMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Ratansner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Ander B., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Blownstein M.J., Usdin T.B., Tornici P., Prange C., Ratapleton M.J., Usdin T.B., Tornici P., Prange C., Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Roha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P. H. RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R.A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rableteild Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences ""

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
"Molecular cloning, expression analysis, and chromosomal localization of mouse Hmg1-containing sequences.";
Manm. Genome 5:91-99(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sclurognathi; Muroidea; Murinae; Mus
                                                                                                                                                                                                                     HWG1 MOUSE STANDARD; PRT; 214 AA.
P63158; P07155; P27109; P27428;
P0.1-APR-1988 (Rel. 07, Created)
01-APR-1998 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv; TISSUB=Liver;
MEDLINE=95050689; PubMed=7961836;
Ferrari S., Ronfand L., Calogero S., Bianchi M.;
Frrmari S., Ronfandi L., Calogero S., Bianchi M.;
"The mouse gene coding for high mobility group 1 protein (HMG1).";
J. Biol. Chem. 269:28803-28808(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yotov W.V., St Arnaud R.; mouse cDNA encoding the nonhistone "Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group protein-1 (HMG1)."; Nucleic Acids Res. 20:3516(392).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghosh B.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                       Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92335012; PubMed=1630928;
                                                                                                               152 EKYEKDIAA 160
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                       61 EKYEKDIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C3H/He;
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norvegicus (Rat)
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   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKKL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P63159; P07155; P27109; P27428; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) High mobility group protein 1 (HMG-1) (High mobility group protein 1 (HMG-1) (High mobility Synonyms-Hmg-1, Hmg1; Name-Hmgb1; Synonyms-Hmg-1, Hmg1;
FUNCTION: Binds preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
                                                           with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material. SIMILARITY: Belongs to the HWGI/HWG2 protein family. SIMILARITY: Concains 2 HWG box DNA-binding domains.
                                                 SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
                                                                                                                                                                                                                                                                                                                   MGI; MGI:96113; Hmgbl.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:uccleus; TAS.
GO; GO:0005615; F:uccleus; TAS.
GO; GO:0005615; F:protein binding; IPI.
GO; GO:0006810; P:nitric.oxide biosynthesis; IDA.
GO; GO:0006810; P:ransport; IDA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR00010; Highmoblty_12.
Pfam; PF00505; HMG Dox; Z.
PFam; PF00505; HMG Dox; Z.
PRINTS; PR00886; HIGHMOBLTY12.
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0
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178 E -> V (in Ref. 4).
189 D -> E (in Ref. 3).
24763 MW; B3C6A91FD6F1B133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 370; DB 1;
Pred. No. 1.7e-31;
                                                                                                                                                                                        EWEL; 211997; CAA78042.1; -; MRNA.
EWEL; U00431; AAA20508.1; -; MRNA.
EWEL; EX0457; CAA5631.1; -; Genomic_DNA.
EWEL; L38477; AAA57042.1; -; MRNA.
EWEL; BC006586; AA406586.1; -; MRNA.
EWEL; BC008565; AA408565.1; -; MRNA.
EWEL; BC085090; AA4083067.1; -; MRNA.
EWEL; BC085090; AA4083067.1; -; MRNA.
EWEL; BC085090; AA408090.1; -; MRNA.
EWEL; BC085090; AA408090.1; -; MRNA.
EWEL; BC085090; AA408090.1; -; MRNA.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005631; C:mcleus; TAS.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
TAPERDED.
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HMG box 1.
HMG box 2.
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78
162
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EKYEKDIAA 160
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8
94 1
185 2
178 1
189 1
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INIT MET
DNA BIND
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CONFLICT
CONFLICT
SEQUENCE
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MEDILINE=9158468; PubMed=1885601;
Medilines J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Morenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
Morenmies J., Pihlaskari Brotein of brain (amphoterin) involved in
neurite outgrowth. Amino acid sequence and localization in the
filopodia of the advancing plasma membrane.";
J. Biol. Chem. 266:16722-16729(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal sequence and production of antipeptide antibodies that detect p30 at the surface of neuroblastoma cells and of brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 34:16596-16607(1995).
-1- FUNCTION: Bands preferentially single-stranded DNA and unwinds double stranded DNA. Heparin-binding protein that has a role in the extension of neurite-type cytoplasmic processes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
MEDLINE=96118376; PubMed=8527432;
Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
Thomas J.O., Laue B.D.;
"Structure of the A-domain of HMG1 and its interaction with DNA as
studied by heteronuclear three- and four-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated with the plasma membrane of filipodia in process-growing cells, and also deposited into the substrate-attached material.
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Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
Thomas J.O.;
"Structure of the HMG box motif in the B-domain of HMGI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney, Prostate, and Teetis;
NIH - Mammalian Gene Collection (MGC) project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bianchi M.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley, TISSUE-Liver,
MEDLINE-88067717; PubMed-3684582;
Paonessa G., Frank R., Cortess R.;
Procleoide sequence of rat liver HMG1 cDNA.";
Nucleic Acids Res. 15:9077-9077 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M64986; AAA40729.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Biol. 107:2293-2305(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 87-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 12:1311-1319(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 1-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 1-83.
                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
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                                                                                                                             NCBI_TaxID=10116;
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1. SPAEH
088611_SPAEH PRELIMINARY;
088611;
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Best Local Similarity 100.
Matches 69; Conservative
                                                               Conservative
                                                                                                                                                 153 EKYEKDIAA 161
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153 EKYEKDIAA 161
                                                                                                                             69
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                                                    Similarity
69; Conserva
                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                          Query Match
Best Local S
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10 088611
AC 08861
DT 01-NG
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DB High
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OC Bukax
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                           PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
3D-structure; Chromosomal protein; Direct protein sequencing; DNA-binding; Heparin-binding; Nuclear protein; Repeat.
INIT MET 0 0 78 HMG box 1.
DNA-BIND 94 162 HMG box 2.
COMPBIAS 185 214 Asp/Glu-rich (acidic).
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. GO; GO:0000785; C:chromatin; IEA. GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                24763 MW; B3C6A91FD6F1B133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1.
Name-HWGB1; ORFNames=RP11-550P23.1-004;
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 370; DB 1;
100.0%; Pred. No. 1.7e-31;
tive 0; Mismatches 0;
                                       PIR; A41175; NSRTH1.
PDB; 1AAB; NWR; @=1-83.
PDB; 1CKT; X-ray; A=7-77.
PDB; 1HMF; NWR; @=88-164.
PDB; 1HMF; NWR; @=88-164.
SMR; P63159; 1-83, 92-170.
Ensembl; ENSRNOG0000030351; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AA.
Y00463; CAA68526.1; -; mRNA.
BC061779; AAH61779.1; -; mRNA.
BC081839; AAH81839.1; -; mRNA.
BC088402; AAH88402.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                            InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; 7.
PRINTS; PR00886; HIGHMOBLTY12.
SWART; SM00398; HMG; 2.
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QST7C3;
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                                                                                                                                                                                                                                                                                                                                                                                                 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                     2802; Hmgb1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Spalacinae; Nannospalax.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation 
13-SEP-2005 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
SEQUENCE 215 AA; 24894 MW; 8A868CP277D417B5 CRC64;
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                                                                                                                                                                                                                                                               Length 215;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                               100.0%; Score 370; DB 2;
100.0%; Pred. No. 1.7e-31;
tive 0; Mismatches 0;
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Pfam; PF00505; HMG box; 2.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
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                                            EKYEKDIAA 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 152
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R GO; GO:00007634; C:chromatin; IEA.

R GO; GO:00005634; C:mucleus; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003675; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R InterPro; IPR00010; HMG 12_box.

R PRINTS; PR00505; HMG box; Z.

R PRINTS; PR00398; HMG; 2.

R PRNSTT; SM0398; HMG; 2.

R PROSITE; PS50118; HMG BOX 2; 2.

C SEQUENCE 215 AA; 24923 MW; 1C6FB6845CAlEGC8 CRC64;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Spalacinae; Nannospalax.
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                                                                                                                                                                                                                                                                              BNR; 088611; 2-84, 93-171.

GO; GO:0000785; C:chrcmatin; IEA.

GO; GO:0000785; C:chucleus; IEA.

GO; GO:000357; F:DNA binding; IEA.

GO; GO:000357; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IRR00185; Highmoblty_12.

PRINTS; PRO0886; HMG_Lox; Z.

PRINTS; PRO0886; HMG_LOX; Z.

PRINTS; PRO0886; HMG; 2.

PROSITE; PS50118; HMG EOX Z; Z.

PROSITE; PS50118; HMG EOX Z; Z.

SEQUENCE 215 AA; Z4905 WW; 64816B6FCF6033EA CRC64;
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                                                                                                                   Lee K.-L.D., Lum H.-K., Nevo E.;
Submitred (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078B17, AAC27650.2; -; Genomic_DNA.
HSSP; P07156; INHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee K.-L.D., Lum H.-K., Nevo E.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078818; AAC27651.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 370; DB 2;
100.0%; Pred. No. 1.7e-31;
tive 0; Mismatches 0;
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NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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RESULT 13
008612 SPA
1008612 SPA
1008611
01-NC
0

Matches

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93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNTAADDKQPYEKKAAKLK 152
                                                                                                                                             Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Eharchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Spalacinae, Nannospalax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridas; Spalacinae; Nannospalax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Lee K.-L.D., Lum H.-K., Nevo E.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AROT8819; AAC27652.1; -; Genomic_DNA.
HSSP; P07156; 1NHN.
SMR; Q9QWY6; 2-84, 93-171.
GO; GO:000785; C:chromatin; IEA.
GO; GO:000785; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000110; HMG_12_box.
Pfam; PF00505; HMG box; 2.
Pfam; PF00505; HMG box; 2.
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0
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO78820; AAC27653.2; -; Genomic_DNA.
HSSP; P07156; INHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PSS0118; HMG BOX 2; 2.
SEQUENCE 215 AA; 24822 MM; D20D659274B575B4 CRC64;
QQQX40_SPAEH PRELIMINARY; PRT; 215 AA.
QQX40;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
High mobility group protein.
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DR SWR; 090X40; 2-84, 93-171.

DR GO; GO:0000785; C:chromatin; IEA.

DR GO; GO:00005634; C:nucleus; IEA.

DR GO; GO:00005634; C:nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR000135; Highmoblty_12.

DR Ffam; PF00505; HMG box; 2.

DR Fram; PF00505; HMG box; 2.

DR PROSITE; PS00139; HMG DOX; 1.

DR PROSITE; PS00139; HMG BOX; 2.

DR PROSITE; PS00139; HMG BOX; 2.

DR PROSITE; PS00139; HMG BOX 1.

DR PROSITE; PS00139; HMG BOX 2; 2.

SQUENCE 215 AA; 24895 WW; 599FB8A6FDF41F17 CRC64;

Auery Match

DR PROSITE; PS00118; HMG BOX 1, 1.

Best Local Similarity 100.0%; Pred. No. 1.7e-31;

Matches 69; Conservative 0; Mismatches 0; Gaps 0;

QY INAPKRPPSAFELFCSEYRPKIKGEHPGLSIGDVAKKIGEMWNNTAADDKQPYEKKAAKLK 60

DD 93 NAPKRPPSAFELFCSEYRPKIKGEHPGLSIGDVAKKIGEMWNNTAADDKQPYEKKAAKLK 152

QY 61 EKYEKDIAA 69

DD 153 EKYEKDIAA 161
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Search completed: April 6, 2006, 10:25:16 Job time : 82.4836 secs

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Sequence 1, Application US/09214881A
Patent No. 6822078
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Gesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
||||||||||
152 EKYEKDIAA 160
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EKYEKDIAA 69
RESULT 2
US-09-214-881A-1
FEATURE:
임
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 883, App Sequence 1, Appli Sequence 4, Appli Sequence 5, Appli Sequence 1018, A Sequence 1018, A Sequence 1018, Appli Sequence 6, Appli Sequence 8, Appli Sequence 10728, Appli Sequence 324, App                                                                       (without alignments)
288.890 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                            April 6, 2006, 10:25:39 ; Search time 19.7467 Seconds
                                                                                                          370
1 NAPKRPPSAFFLFCSEVRPK......QPYEKKAAKLKEKYEKDIAA
        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/s_COMB.pep:*
/cgn2_6/ptodata/1/iaa/s_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                               572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                US-10-717-984-5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                    Scoring table:
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                                                                                                                   Sequence:
                                                                                                                                                               Searched:
                                                             Run on:
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Sequence 789, App
Sequence 324, App
Sequence 324, App
Sequence 324, App
Sequence 1667, Ap
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Sequence 10496, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-538-092-883
i Sequence 883, Application US/09538092
j Patent No. 675314
j GENERAL INFORMATION:
i APPLICANT: Giot, Loi C.
i APPLICANT: Mansfield, Traci A.
j TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 1596-542
j CURRENT APPLICATION NUMBER: US/09/538,092
j PRIOR APPLICATION NUMBER: 60/127,352
j PRIOR FILING DATE: 2000-03-29
j PRIOR FILING DATE: 2000-03-29
j PRIOR FILING DATE: 2000-02-01
j RIOR FILING DATE: 2000-02-01
j PRIOR FILING DATE: 2000-02-01
j RIOR FILING DATE: 2000-02-01
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LOCATION: (0)...(0)
CTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883-901-89
                         US-09-651-563-324
US-09-651-563-389
US-09-519-642-389
US-09-705-1667
US-09-705-1667
US-09-614-1248-1667
US-09-671-325-1667
US-09-671-325-1667
US-10-017-754-1667
US-10-017-754-1913
US-09-651-563-1667
US-09-651-563-1667
US-09-61-563-1667
US-09-61-610-10496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 370; DB 2; Best Local Similarity 100.0%; Pred. No. 3.1e-40; Matches 69; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-814-964-7
US-08-258-442-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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Ozaki, Shoichi
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US-09-214-881A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09214881A

Patent No. 6822078

GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Osayi, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Shirdaka, Michiteru
APPLICANT: Osakada, Pumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06838401044
CURRENT FILING DATE: 1999-06-07

CURRENT PILING DATE: 1999-06-07
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                                                                                                                                                                                                                                                                                                                                          Length 214;
           APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Score 370; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0;
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100.0%; Score 370; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0;
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; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
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Nakao, Kazuwa
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152 EKYEKDIAA 160
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152 EKYEKDIAA 160
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ORGANISM: Homo sapiens
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; ORGANISM: Bos taurus
US-09-214-881A-3
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SEQ ID NO 3
LENGTH: 214
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US-09-214-881A-3
                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 214
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92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKHPYEKKAAKLK 151
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APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Ususuji, Hiroko
APPLICANT: Ususuji, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Punko
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06833.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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                                                                                                                                                  Shirakawa, Hitoshi
Osakada, Fumio
NVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6%; Score 365; DB 2; Length 214; Best Local Similarity 98.6%; Pred. No. 1.4e-39; Matches 68; Conservative 0; Mismatches 1; Indels
                                                                 APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTY
FILE REFERENCE: 069383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 214
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Sobajima, Junko
Uesugi, Hiroko
Okazaki, Takahiro
Tanaka, Masao
Nakao, Kazuwa
Yoshida, Michiteru
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ORGANISM: Sus scrofa
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SEQ ID NO 5
LENGTH: 214
TYPE: PRT
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92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151
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APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Obasada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383,0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
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APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
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Pred. No. 3e-34;
4; Mismatches 5; Indels
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Shoichi
APPLICANT: Usugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Useugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
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ilarity 87.0%;
Conservative
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Best Local Similarity 87.0%;
Matches 60; Conservative
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152 EKYEKDIAA 160
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61 EKYEKDIAA 69
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ORGANISM: Homo sapiens
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SOFTWARE: Patentin Ver
SEQ ID NO 6
LENGTH: 209
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Best Local Similarity
Matches 60; Conserv
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US-09-214-881A-6
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SEQ ID NO 2
LENGTH: 208
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                               ; Sequence 10013, Application US/09949016
; Patent No. 6812339
; GENERAL INCORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REPRENCE: CLOOL307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-01-08
; PRIOR FILING DATE: 2000-01-08
; RIOR RELING DATE: 2000-01-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTMARE: PESALSEQ for Windows Version 4.0
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
TITLE OF INVENTION:
FILE REPRENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 96.2%; Score 356; DB 2; Length 213;
1 Similarity 97.1%; Pred. No. 2.1e-38;
67; Conservative 0; Mismatches 2; Indels
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; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
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PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatsedFormatter Version 0.9
SEQ ID NO 1018
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155 EKYEKDIAA 163
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 67; Conserv
                          US-09-949-016-10813
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US-09-538-092-1018
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US-09-214-881A-9
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| Sacquence 10728, Application US/09949016
| Patent No. 6812339
| GENERAL INPORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR FILING DATE: 2000-09-08
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFFWARE: PESEC FOR Windows Version 4.0
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                         92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151
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1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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87.0%; Pred. No. 3e-34;
tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                            Sequence 8, Application US/09214881A
Patent No. 6822078
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
SAPLICANT: Sobajima, Junko
APPLICANT: Osavaji, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Yoshida, Michiteru
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152 EKYEKDIAA 160
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                                                                                       EKYEKDIAA 69
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Matches 60; Conserva
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ORGANISM: Human
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LENGTH: 320
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LENGTH: 209
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92 NAPKRPPSAFFLFCSEHRPKIKNDHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151
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APPLICANT: Sobajina, Junko
APPLICANT: Sobajina, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Yoshida, Michiteru
APPLICANT: Shida, Michiteru
APPLICANT: Shida, Michiteru
APPLICANT: Shida, Michiteru
APPLICANT: Osakada, Punio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
TITLE REFERENCE: 06838:0104
CURRENT APPLICATION NUMBER: US99-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 206
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Score 324; DB 2; Length 320;
Pred. No. 5.1e-34;
4; Mismatches 5; Indels
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Sequence 38, Application US/09914259

Sequence 38, Application US/09914259

Patent No. 6495336

GENERAL INFORMATION:

APPLICANT: MANANATION:

APPLICANT: Hyman, Paul

APPLICANT: Williams, Mark

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999

CURRENT FILING DATE: 2000-11-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 879
    Query Match
Best Local Similarity 87.0%;
Matches 60; Conservative
                                                                                                                                                                                                              264 EKYEKDIAA 272
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; ORGANISM: Homo sapiens
US-09-914-259-38
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APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: Liqun
TITLE OF LIVE DATE: 2009:10-30
NUMBER OF SEQ 1D NOS: 1833
                                                                                                                                                                                                                                                                                                                           APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Oseugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Michiteru
APPLICANT: Yoshida, Michiteru
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Funio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.010
FILE REFERENCE: 1999-06-07
CURRENT APPLICANTON UMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
SEQ ID NO 10
LENGTH: 201
TYPE: PPF
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Query Match 85.7%; Score 317; DB 2; Length 879; Best Local Similarity 88.4%; Pred. No. 1.5e-32; Matches 61; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 81.1%; Score 300; DB 2; Length 201; 1 Similarity 79.4%; Pred. No. 3.9e-31; 54; Conservative 6; Mismatches 8; Indels
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827 EKYKKDIAA 835
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ORGANISM: Gallus gallus
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150 EKYEKDVA 157
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Matches 54; Conserva
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; SEQ ID NO 324
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-324

Query Match
Best Local Similarity 79.4%; Pred. No. 2.4e-30;
Matches 54; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
Qy 1 NAPKRPPSAPFLFCSEYRPKIKGHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
Db 91 NAPKRPPSGFFLFCSERPRIKSTNPGISIGDVAKKLGEMWNNLNDSEKQPYITKAAKLK 150
Qy 61 EKYEKDIA 68
Db 151 EKYEKDIA 68
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Publication No. US2030144201A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
APPLICANT: Huan Yang
APPLICANT: Mitchell P. Fink
ITILE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
TITLE OF INVENTION: USE OF UNDER SERVICE OF USER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-147-447-5

Sequence 5, Application US/10147447

Publication No. US20030060410A1

GENERAL INFORMATION:

APPLICANT: Tracey, Kevin J.

APPLICANT: Tang, Huan

APPLICANT: Fink, Mitchell P.

TITLE OF INVENTION: Use of HMG Fragments as

TITLE OF INVENTION: Anti-Inflammatory Agents

FILE REFERENCE: 3268.1001-001

CURRENT APPLICATION NUMBER: US/10/147,447

CURRENT FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 69
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US-10-938-992-74
US-10-087-192-1443
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US-10-868-577A-63
US-10-868-549-22
US-10-938-992-18
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US-10-718-495-2
US-10-717-984-1
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ORGANISM: Homo sapiens
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EKYEKDIAA 69
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Best Local Similarity
Matches 69; Conserv
RESULT 2
US-10-300-072-5
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Sequence 1, Appli
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1 NAPKRPPSAFFLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA
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/cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-300-072-5
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US-10-456-947-5
US-10-718-495-5
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US-10-718-495-51
US-10-938-992-76
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US-10-087-192-1446
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Minimum DB Maximum DB

Database

Result 8

Searched:

9 9

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FILE REFERENCE: 3268.1001-007
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Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

APPLICANT: Huan Yang

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
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                                                                                                                                                                                                                                                                           Length 69;
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                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                    ch 100.0%; Score 370; DB 4; Similarity 100.0%; Pred. No. 5.5e-37; 69; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10456949

Publication No. US20040005316A1

GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3268.1001.006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT APPLICATION NUMBER: 10/10/456,949
FRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
SEQ ID NOS: 23
SOFTWARE: FABSEG for Windows Version 4.0
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR PLICATION NUMBER: US 60/291,034
PRIOR PLILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 5
LENGTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
TYPE: PRI
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
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Best Local Similarity
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Matches 69; Conserva
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US-10-456-949-5
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US-10-456-947-5
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1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMMNNTAADDKQPYEKKAAKLK 60
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Pred. No. 5.5e-37;
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Sequence 5, Application US/10718495

Publication No. US20040141948A1

GENERAL INFORMATION:

APPLICANT: O'Keefe, Theresa L.

TITLE OF INVENTION: USE OF HUGGE FRAGMENTS AS

TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

FILE REFERENCE: 3258.1009-001

CURRENT APPLICATION NUMBER: US/10/718,495

CURRENT APPLICATION NUMBER: 60/427,841

PRIOR FILING DATE: 2002-11-20
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US-10-717-984-5
Sequence 5, Application US/10717984
Publication No. US20040156851A1
GENERAL INFORMATION:
APPLICANT: Newman, Walter
TITLE OF INVENTION: HARBI COMBINATION THERAPIES
FILE REFERENCE: 3288.1008-001
CURRENT APPLICATION NUMBER: US/10/717,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
CURRENT APPLICATION NUMBER: US/10/456,947
CURRENT FILING DATE: 2003-06-06
FRIOR APPLICATION NUMBER: 10/147,447
FRIOR FILING DATE: 2002-05-15
FRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
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Best Local Similarity 100.0%;
Matches 69; Conservative 0;
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FILE REFERENCE: 3268.1001-007
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US-10-718-495-51
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Matches
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Publication No. US20040053841A1
GENERAL INFORMATION.
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: HAGE POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
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Sequence 51, Application US/1030072

Bublication No. US20030144201A1

GENERAL INFORMATION:
APPLICANT: Hean Yang
APPLICANT: Hean Yang
APPLICANT: Heal Yang
APPLICANT: Heal Yang
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
TITLE OF INVENTION: USE OF HMGB FRAGMENTS
FILE REFERENCE: 3268.1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 60/291,034
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 74
                                                                                                                                                                                                                                           100.0%; Score 370; DB 4; Length 69; 100.0%; Pred. No. 5.5e-37; ive 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,846
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 69
                                                                                                                                                                                                                                                                                      69; Conservative
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61 EKYEKDIAA 69
                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-300-072-51
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Matches 69; Congerm
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US-10-300-072-51
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US-10-456-947-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQUENCE 51, Application US/10718495
PUblication No. US20040141948A1
GENERAL INFORMATION:
APPLICANT: O'Reefe, Theresa L.
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
PRIOR PAPLICATION NUMBER: 60/427,841
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR APPLICATION NUMBER: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SEQ ID NOS: 58
LENGTH: 74
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CURRENT APPLICATION NUMBER: US/10/456,947
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR PRILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
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                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
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CORGANISM: Homo sapiens
US-10-718-495-51
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65 EKYEKDIAA 73
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61 EKYEKDIAA 69
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Publication No. US20050152903A1

GENERAL INFORMATION:
APPLICANT: Newman, Walter
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Keefe, Theresa
APPLICANT: O'Sobert
TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
FILE REFERENCE: 3258.1033-001
CURRENT FILING DATE: 2004-09-10

CURRENT FILING DATE: 2004-09-11

PRIOR APPLICATION NUMBER: 60/502,568

PRIOR FILING DATE: 2003-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence (7, Application US/10938992)

Publication No. US20050152903A1

GENERAL INFORMATION:
APPLICANT: Newman, Walter
APPLICANT: Qim, Shixin
APPLICANT: O'Reefe, Theresa
APPLICANT: O'Dar, Robert
ITILE OF INVENTION: Monoclonal Antibodies Against HWGB1
FILE REFERENCE: 3258.1033-001
CURRENT FILING DATE: 2004-09-10
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 74
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Best Local Similarity 100.
Matches 69; Conservative
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EKYEKDIAA 73
                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 69; Conserval
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US-10-938-992-76
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US-10-938-992-67
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                                                             SEQ ID NO 51
LENGTH: 74
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Publication No. US20040053841A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: HAGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REPERENCE: 3268.1001-007
CURRENT APPLICATION NUMBER: US/10/456,947
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## SAPPLICANT: Kevin J. Tracey
## APPLICANT: Han Yang
## APPLICANT: Han Yang
## APPLICANT: Han Yang
## APPLICANT: Han Yang
## APPLICANT: Hitchell P. Fall
## APPLICANT: Mitchell P. Fall
## APPLICANT: Mitchell P. Fall
## TITLE OF INVENTION: AGENTS
## TITLE OF INVENTION NUMBER: US/10/300,072
## CURRENT FILING DATE: 2002-01-120
## PRIOR PAPLICATION NUMBER: US 60/291,034
## PRIOR FILING DATE: 2001-05-15
## NUMBER OF SEQ ID NOS: 58
## SOFTWARE: FastSEQ for Windows Version 4.0
## SEQ ID NO 58
## ILENGTH: 92
## ILENGTH: 93
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; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-76
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Publication No. US20030144201A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 69; Conservative
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1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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US-10-718-495-58
Sequence 58 Application US/10718495
Publication No. US20040141948A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
PRIOR PAPLICATION NUMBER: 60/427,841
PRIOR PAPLICATION NUMBER: 60/427,841
PRIOR PILING DATE: 2003-11-12
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FARESEQ for Windows Version 4.0
LENGTH: 92
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-43
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ORGANISM: Homo sapiens
US-10-718-495-58
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65 EKYEKDIAA 73
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65 EKYEKDIAA 73

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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-821-234-1443
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Sequence 11, Appl
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Sequence 192, Appl
Sequence 26884, Ap
Sequence 26881, Ap
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8838, Ap
3073, Ap
869, App
9518, Ap
3510, Ap
1571, Ap
9185, Ap
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4976, Ap
12564, Ap
10060, A
9681, Ap
9680, Ap
32735, A
32734, A
1105, Ap
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                                                                                                                                                  April 6, 2006, 10:28:08; Search time 8.625 Seconds (without alignments) 249.536 Million cell updates/sec
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Sequence 1
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1 NAPKRPPSAPPLFCSEYRPK......QPYEKKAAKLKEKYEKDIAA
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4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Van
APPLICANT: Ardarmani, Susan
APPLICANT: Tang, Y. Tom
TILLE OF INVENTION Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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US-11-096-568A-15614
US-11-097-099-7055
US-11-087-099-713
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US-11-172-740-1565
US-11-172-740-1565
US-11-172-740-1566
US-11-172-740-1566
US-11-124-168A-309
US-11-124-368A-309
US-11-124-368A-310
US-11-124-368A-310
US-11-124-368A-310
US-11-1096-568A-21033
US-11-096-568A-21033
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US-11-172-740-1570
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Publication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Circleal Theresa
APPLICANT: Unclano, Peter
APPLICANT: Qin, Shixin
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258.1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT APPLICATION NUMBER: 05/599,678
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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RESULT 6
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                                                                                                                                                                                                                                                                       Length 215;
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100.0%; Score 370; Dength 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0;
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Publication No. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: O'Keefe, Theresa
APPLICANT: Uctiano, Peter
APPLICANT: Uctiano, Peter
APPLICANT: O'Keefe, Theresa
FILE REFERENCE: 3288.1021-003
CURRENT APPLICATION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3288.1021-003
CURRENT APPLICATION WUMBER: US/11/186,422
CURRENT FILING DATE: 2005-07-20
FRIOR APPLICATION NUMBER: 60,589,678
FRIOR PRICATION NUMBER: 60,589,678
FRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 215
TYPE: PRT
CREANISM: Home sapiens
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; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION: Therapeutics, Inc.
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: Usciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RASE PROTEIN DERIVATIVES
; TITLE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
CURRENT FILING DATE: 2004-04-07
PRIOR PEDLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQTWARE: DE SEQ_Genes Version 1.0
SEQ ID NO 1443
LENGTH: 215
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153 EKYEKDIAA 161
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CORGANISM: Homo sapiens
US-10-821-234-1443
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Section 192, Application US/11169041

| Sequence 192, Application US/11169041
| Publication No. US20060019284A1
| GENERAL INFORMATION:
| APPLICANT: Bristol-Myers Squibb Company
| TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION: CELLS
| FILE REFERENCE: 10001 NP
| CURRENT APPLICATION NUMBER: US/11/169,041
| CURRENT APPLICATION NUMBER: 60/584,405
| PRIOR FILING DATE: 2004-06-30
| WINDER OF SEQ ID NOS: 527
| SEQ ID NO 192
| SEQ ID NO 192
| LENGTH: 879
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Publication No. US20050255114A1
GENERAL INPORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: And Y. Tom
APPLICANT: And Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-07
PRIOR APPLICATION NUMBER: US 60/462,047
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/589,678
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 215
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||||
153 EKYEKDIAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     827 EKYKKDIAA 835
                                                                                                                                                                                          ORGANISM: Mus musculus US-11-186-422-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EKYEKDIAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-11-169-041-192
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                                                                                                                                                                                                                 Length 187;
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Best Local Similarity 47.1%; Pred. No. 8e-13;
Matches 32; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8838, Application US/11087099
Publication No. US20060041961A1
EMBERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3073, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
44.5%; Score 164.5; DB 7;
Best Local Similarity 47.1%; Pred. No. 1.5e-12;
Matches 33; Conservative 12; Mismatches 24;
                                                                                                                                                                                                               45.5%; Score 168.5; DB 7; 48.4%; Pred. No. 7.1e-13;
                                    TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1). (187)
OTHER INFORMATION: Ceres Seq. ID no. 13627625
                                                                                                                                                                                                             Query Match 45.5%; Score 168.5; \nu Best Local Similarity 48.4%; Pred. No. 7.1e-Matches 31; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Canavalia gladiata
US-11-087-099-3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Candida albicans
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77 KRYEKEKA 84
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                                                                                                                                                                         US-11-096-568A-26883
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US-11-087-099-8838
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US-11-087-099-3073
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SEQ ID NO 26883
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Publication No. US20060048240A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 2760-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 26884
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Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION WUMBER: US/11/096,568A

CURRENT APPLIAND DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                                                                                                                                           11; Indels
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48.4%; Pred. No. 5e-13;
iive 13; Mismatches 19;

    LOCATION: (1)...(169)
    OTHER INFORMATION: Xaa = any amino acid or nothing
    US-10-821-234-1234

                                                                                                                                                                                                                                                                            Score 279; DB 6;
Pred. No. 3.7e-26;
6; Mismatches 11;

    LOCATION: (1)...(139)
    OTHER INFORMATION: Ceres Seq. ID no. 13627626
US-11-096-568A-26884

                    NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1234
LENGTH: 169
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 75.0%;
Matches 51; Conservative
  PRIOR FILING DATE: 2003-04-07
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Matches 31; Conservative
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140 EEYGKDFA 147
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US-11-096-568A-26883
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US-11-096-568A-26884
                                                                                                                                                                                             LOCATION:
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US-11-087-099-3510
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LENGTH: 149
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  NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
                        1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.1%; Score 163; DB 7; Length 93; Best Local Similarity 45.5%; Pred. No. 1.4e-12; Matches 30; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-11-087-099-9518

i Sequence 9518, Application US/11087099
i Publication No. US20060041961A1
i GENERAL INFORMATION:
i APPLICANT: Abad, Mark S. et al.
i TITLE OF INVENTION: Genes and Uses for Plant Improvement
i FILE REFERENCE: 38-21(53450)B EP
i CURRENT APPLICATION NUMBER: US/11/087,099
i CURRENT PILING DATE: 2005-03-22
i NUMBER OF SEQ ID NOS: 12464
i SEQ ID NO 9518
                                                                                                                                                                                                                      Sequence 869, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B.FP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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CTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-9518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Saccharomyces cerevisiae
                                                                                                         ||:|:| | |
KEEYDKSILA 104
                                                                                KEKYEKDIAA 69
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KRYESE 84
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KRYESE 84
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Sequence 1571, Application US/11172740

Publication No. US2066057724A1

GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: UNCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR A TITLE OF INVENTION: UNBER: US.11/172,740

CURRENT APPLICATION NUMBER: US.11/172,740

CURRENT FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 2523

SEQ ID NO 1571

LENGTH: 149
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OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: Utility: Useful for making ornamental plants with modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 NKPKRPPSAFFVFMADFREQYKKDHPNNKSVAAVGKACGEEWKSLSEEEKAPYVDRALKK 102
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Sequence 3510, Application US/11087099
Publication No. US20060041961A.
Publication No. US20060041961A.
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement TILLE REFERENCE: 38-21(53450) B.P.
CURRENT FILIAN NUMBER: US/11/087,099
CURRENT FILIAN DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.9%; Score 162.5; DB 7; Best Local Similarity 44.3%; Pred. No. 2.8e-12; Matches 31; Conservative 14; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
FEATURE:
LOCATION: (1)...(149)
OTHER INFORMATION: Public GI no. 729737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .03 KEEYEITLQA 112
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LOCATION:
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Vicia faba
US-11-087-099-3510
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US-11-172-740-1571
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OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
                                                                                                          ; OTHER INFORMATION: Utility: Useful for making plants with increased biomass US-11-172-740-1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                                                               Query Match
43.9%; Score 162.5; DB 7; Length 149;
Best Local Similarity 44.3%; Pred. No. 2.8e-12;
Matches 31; Conservative 14; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
43.1%; Score 159.5; DB 7; Length 141;
Best Local Similarity 44.3%; Pred. No. 6.1e-12;
Matches 31; Conservative 13; Mismatches 25; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **Sequence 9185, Application US/11087099

; Sequence 9185, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REPERSING: 38 = 21 (53450) B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT PILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 9185

; LENGTH: 141
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Job time : 9.625 secs
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SUMMARIES	ID Description	AAE35864 Aae35864 Human HMG	ADO25940 Ado25940 Tumour ne	ADO71499 Ado71499	AAE35868 Human HMG	AD025937 Ad025937 Human hig	AD025958 Ado25958 High mobi	AD071496 Human	AD071529 Human	ADY85364 Human	ADY85333 Aigh n	ADY85080 Ady85080 1	ADY85014	AAE35867	AD025936 Human	AD071495 Ado71495	ADY85379 Ady85379 Human	ADP3 003 0	AAE35866	ADO25935 Ado25935 Wild type	AD025941 Human	ADO71494 Humar	ADO71500 Human	ADY85335 High	
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Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis; allery; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer's disease; Goodpasture's syncardial ischaemia; diabetes; annoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene therapy; human immunodeficiency virus; HMGBI protein. (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO) GEN HOSPITAL CORP. (UYPI-) UNIV PITTSBURGH. MP; Fink AAE35864 standard; peptide; 20 AA. Warren HS, Human HMG1 B box fragment #1. 15-MAY-2002; 2002WO-US015329. 15-MAY-2001; 2001US-0291034P. (first entry) Yang H, WPI; 2003-120594/11. WO200292004-A2. Homo sapiens. 17-JUN-2003 21-NOV-2002. Tracey KJ, AAE35864; AAE35864

New isolated polypeptide having a vertebrate HMG A box, useful for inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.

Example 4; Page 45; 82pp; English.

The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-

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              cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, bronchitis, emphysema, HV infection, candidiasis, malaria, filariasis, amoebiasis, dermatitis, therosclerosis, Alzheimer's disease, myocarditis, myocarditis, meningitis, multiple sclerosis, gout, erefebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMG1 (also termed as HMGB1) B box
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naturally occurring HMG A box inhibits the release of a pro-inflammatory
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iive 0; Mismatches 0;
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immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of tumour necrosis factor

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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the collypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; high mobility group box 1 B box; HMGB1 B box; HMGB; HMGB A box, HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Baccet si disease; graff-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human high mobility group box 1 (HMGB1) B box protein active fragment #2.
(TNF) stimulating peptide based on amino acids 1-20 of the human high mobility group box 1 (HMG1) protein.
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20-NOV-2002; 2002US-0427846P.
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rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versuse-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGBI B box polypeptide active fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; appendicitis; peptic ulcer; duodenal ulcer; crohn's disease; meningitis; allery; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer; a disease; Goodpasture's syndrome; graff-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene_therapy; human immunodeficiency virus; HMGBI protein; mutant;
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iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HMG1 protein mutant #2.
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The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a non-naturally occurring HMG A box inhibites the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's

Example 1; Page 37; 82pp; English.

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         sinusitis, bronchitis, emphysem, HIV infection, candidisais, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocarditis, myocarditis, myocarditis, myocarditis, moritis, goodpasture's myotane, garaft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMG1 (also termed as HMGB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual. The composition individual in need of immunostimulating or increasing an immune response in an individual. This is the amino acid sequence of a human high mobility group box 1 (HMG1) B box mutant.
disease, peritonitis, hepatitis, asthma, allergy, immune complex disease
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HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity;
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(first entry)

26-AUG-2004

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Human; high mobility group box 1, HMGB1, HMGB, HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; asthms; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
                                                             Human high mobility group box 1 (HMGB1) mutant protein #2.
                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003; 2003WO-US037507.
                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2002; 2002US-0427841P.
                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2002; 2002US-0427846P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newman W, O'keefe TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-420628/39.
                                                                                                                                                                                                                                                                                             WO2004046345-A2.
                                                                                                                                                                                                                   mutant; mutein
                                                                                                                                                                                                                                                                                                                           03-JUN-2004
                                                                                                                                                                                                                                                                  Synthetic.
    ADO71496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.
                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; vaccine; pharmaceutical composition;
HMGB B box; high mobility group; immune response; immunostimulation;
cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HMGB B box or its functional variant, sitimulating or increasing an immune response in an individual in need of immunostimulation, and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of human high mobility group box 1 (HMGI) B box biologically active fragment.
                                  Gaps
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    Length 74;
                               Indels
                                                                                                                                                                                                                                                            High mobility group box 1 B box fragment segid 41.
100.0%; Score 110; DB 8;
100.0%; Pred. No. 8.9e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 41; 68pp; English.
                                                                                                                                                                    AD025958 standard; peptide; 74 AA
                                                             1 FKDPNAPKRLPSAFFLFCSE 20
                                                                             1 FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                                 (first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     WO2004046338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                               26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracey KJ;
                                                                                                                                                                                                 AD025958;
                                                                                                                                      RESULT 6
ADO25958
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(CRIT-) CRITICAL THERAPEUTICS INC.

sapiens.

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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinfilammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinfilammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obseity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obseity and conditions characterised by activation of a polypeptide. The polypeptides and conditions characterised by activation of a cuseful in treating obseity and conditions characterised by activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an inflammatory cytokine cascade, e.g. sepais, allograft rejection, rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, mycardial ischaemia, organic ischaemia, reperfusion ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, ulcerative colitis, multiple sclerosis or cachexia. This sequence represents a human HMGB1 mutant polypeptide of the invention.
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100.0%; Pred. No. 8.9e-09;
ive 0; Mismatches 0;
Example 1; SEQ ID NO 20; 113pp; English.
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Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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Indels

100.0%; Score 110; DB 8; 100.0%; Pred. No. 8.9e-09; iive 0; Mismatches 0;

100.08; PL.

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Matches

Local Similarity

Query Match

20

1 FKDPNAPKRLPSAFFLFCSE

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1 FKDPNAPKRLPSAFFLFCSE 20

ADO71496 standard; protein; 74 AA.

RESULT 7 ADO71496 ID ADO7.

Length 74;

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Disclosure; SEQ ID NO 53; 113pp; English
       ADO71529 standard; protein; 74 AA
                                                                                                                          (CRIT-) CRITICAL THERAPEUTICS INC.
                                                                                                      20-NOV-2003; 2003WO-US037507.
                                                                                                             20-NOV-2002; 2002US-0427841P.
20-NOV-2002; 2002US-0427846P.
                        (first entry)
                                                                                                                                   O'keefe TL;
                                                                                                                                          WPI; 2004-420628/39.
                                                                                     WO2004046345-A2.
                                                                                                                                                                                                                                                                             Sequence 74 AA;
                        26-AUG-2004
                                                                                              03-JUN-2004.
                                                                                                                                   Newman W,
                AD071529;
RESULT 8
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The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytckine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to non-B box epitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for effecting weight loss or treating obesity in a patient, a method of determining whether a compound inhibits inflammation, a pharmaccutical compressing an HMGB protein or an antibody that binds to the protein, an agent that inhibits TMF biological activity and a method of treating a condition in a patient characterised by activation of an inflammatory cytokine cascade. Effecting weight loss or treating obesity in a patient comprises administering to the patient an amount of the polypeptide. The polypeptide, antibodies, composition and methods are useful in treating obesity and conditions characterised by activation of such and conditions characterised by activation of an apatient characterised by activation of the polypeptide. The polypeptide and conditions characterised by activation of
                                                                                                                   Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatorid arthritis; asthma; lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pencreatitis; reperitorits; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
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Human high mobility group box (HMGB) B box protein #3
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The invention is based on the discovery that high mobility group box protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when administered with an antigen, diminishes the antibody response to the administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B boxes. A claimed method of treating an immune pathology in an individual comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunesuppressive fragment of the vertebrate or non-natural HMGB A box. The immune pathology is induced by the administration of a non-human antigen, non-adjuvant to the individual, by the transplantation of an organ into the individual, or by infection from a microorganism. Claimed methods of individual, or by infection from a microorganism. Claimed methods of pathology in an individual or decreasing an immune pathology, inhibiting an immune pathology in an individual or decreasing an immune response to an administered non-human antigen comprise administering a HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural A box.

Comprises administering a HMGB polypeptide comprising a vertebrate HMGB A box, or an immunosuppressive fragment of the vertebrate or non-natural HMGB B cox, an ann-maturally-occurring HMGB B cox, an animunosuppressive fragment of these, and a vertebrate or non-naturally boccurring HMGB B cox. The HMGB polypeptide is preferably a HMGBI peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitie, Crohn's disease, asthma, rheumatoid arthritis, ulcerative colitie, crohn's disease, asthma, rheumatoid arthritis, sequence is that of the B box of human HMGILIO, a HMGB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its
                                                                                                                                                                                                                                                                                                                                      High mobility group box; HWG1L10; immune disorder; infection; immunosuppressive; autoimmune disease; allergy; antiallergic; ulcerative colitis; antiinflammatory; antiuleer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiasthmatic; psoriasis; rheumatoid arthritis; antitheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
                                                                                                                                                                                                                                                                                              Human high mobility group box protein HMG1L10 B box.
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                                                                                                                                                          ADY85364 standard; protein; 74 AA
1 FKDPNAPKRLPSAFFLFCSE 20
                          FKD PNA PKRLPSAFFLFCSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
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Gaps

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100.0%; Score 110; DB 8; Length 74; 100.0%; Pred. No. 8.9e-09; tive 0; Mismatches 0; Indels

20; Conservative

Best Local Similarity Matches 20; Conserv

Query Match

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or an immunosuppressive fragment of the vertebrate or non-natural A box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating an immune pathology in an individual comprises administering an amount of a high mobility group box (HMGB) polypeptide comprising a vertebrate or a non-naturally occurring HMGB A or B box, or its
                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; autoimmune disease, antiallergic; ulcerative colitis; autoimmune disease; antiallergic; ulcerative colitis; antialfammatory; antiulcer; gastrointestinal-gen.; Crohns disease; inflammation; asthma; antiasthmatic; rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis; antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer; mutein.
                                                                                     Gaps
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                                                     Length 74;
                                                                                                                                                                                                                                                                                                                                                                                          High mobility group box; HMGB1; immune disorder; infection;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                       High mobility group box protein HMGB1 B box mutant.
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                                                 100.0%; Score 110; DB 9;
100.0%; Pred. No. 8.9e-09;
ive 0; Mismatches 0;
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(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
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                                                                                                                                                                                                                                                 ADY85333 standard; protein; 74 AA
                                                                                                                        1 FKDPNAPKRLPSAFFLFCSE 20
                                                                                                                                            FKDPNAPKRLPSAFFLFCSE 20
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                                                                                                                                                                                                                                                                                                                     (first entry)
                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Warren HS, Tracey KJ;
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                Sequence 74 AA;
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Rattus sp.
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A claimed method of treating an autoimmune disorder in an individual comprises administering at HMGB polypeptide comprising a vertebrate HMGB box, a non-naturally-occurring HMGB A box, or an immunosuppressive fragment of these, and a vertebrate or non-naturally-occurring HMGB B box. The HMGB polypeptide is preferably a HMGB polypeptide is preferably a HMGB be peptide and may be truncated at the C-terminus. The autoimmune disease is allergy, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, sportasis or systemic lugus erythematosus (all claimed). The present sequence is that of a mutated B box of human, mouse and rat HMGBI proteins ADY85326-ADY85327, which was produced in an example from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High mobility group box; HWGB1; monoclonal antibody; antibody therapy, sepsis, antiboacterial immunosuppressive; graff rejection; arthritis; antiarthritic; asthmatic; lupus erythematosus; antiantlanmatory; inflammation; dermatological; respiratory distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress syndrome; respiratory-distress; parcinetic; chronic obstructive pulmonary disease; panoreatitis; peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; asstrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 110; DB 9;
100.0%; Pred. No. 8.9e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2004; 2004WO-US029527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-233483/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HMGB1 A box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005026209-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADY85080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADY85080

110

ADY85080

120

ADY8

AX

ADY8

AX

ADY8

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Thu Apr

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polypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HWGB polypeptide in a sample. The antibody for antigenbinding fragment) binds to a vertebrate HWGB A box but does not specifically bind to non-A box epitopes of HWGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HWGB crotein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsies, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease, graft versus host disease, inflammatory bowel disease, multiple sclerosis and cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HWGB1 APY85012. An identical
 High mobility group box; HMGB1, monoclonal antibody; antibody therapy; sepsis, antibacterial immunosuppressive; graft rejection; arthritis; antiarthritic; asthma; antiasthmatic; lupus erythematosus; antiarthanial erythematosus; antiinflammatory; inflammation; dermatological; respiratory distress syndrome; respiratory-gen.; psoriasis; antipsoriatic; chronic obstructive pulmonary disease; pancreatitis; peritoritis; burns; vulnerary; ischemia; vasotropic; Behcets disease; graft versus host disease; inflammatory bowel disease; gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia; anabolic; infection; musculoskeletal disease; immune disorder.
 New antibody or its antigen-binding fragment specific to a vertebrate high mobility group box (HMGB) A box that inhibits release of a proinflammatory cytokine from a cell treated with HMGB protein, useful for treating, e.g. sepsis.
 100.0%; Score 110; DB 9; Length 74; 100.0%; Pred. No. 8.9e-09; tive 0; Mismatches 0; Indels
 Newman W, Qin S, Okeefe T, Obar R;
 (CRIT-) CRITICAL THERAPEUTICS INC.
 ADY85014 standard; protein; 74 AA
 1 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 11-SEP-2003; 2003US-0502568P.
 10-SEP-2004; 2004WO-US029527
 (first entry)
 Local Similarity 100.
les 20; Conservative
 WPI; 2005-233483/24.
 Human HMGB1 A box.
 WO2005026209-A2.
 Sequence 74 AA;
 16-JUN-2005
 Homo sapiens
 24-MAR-2005.
 Rattus sp.
 ADY85014;
 Query Match
 gb
 ADY855014
ADY855014
ADY855014
AC ADY85
XX
AC ADY85
DT 16-JU
XX
M High
KW Antiph
KW Ant
 Matches
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Disclosure; SEQ ID NO 2; 123pp; English

Gaps ö

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that bind to a vertebrate high mobility group box (HMGB) polypeptide, to methods of detecting and/or identifying an agent that binds to an HMGB colypeptide, methods of treating a condition in a subject characterized by activation of an inflammatory cytokine cascade, and methods of detecting an HMGB polypeptide in a sample. The antibody (or antigenbinding fragment) binds to a vertebrate HMGB hox but does not specifically bind to non-A box epitopes of HMGB, and inhibits release of a proinflammatory cytokine from a vertebrate cell treated with an HMGB coprotein. A method of treating a condition characterized by activation of an inflammatory cytokine cascade comprises administering an antibody of the invention, or its antigen-binding fragment. The condition is selected from sepsis, allograft rejection, arthritis, asthma, lupus, adult respiratory distress syndromic obstructive pulmonary disease, psoriasis, peritonitis, burns, ischemia, Behcet's disease, psoriasis, peritonitis, burns, ischemia, Behcet's disease, cand cachexia, especially sepsis, arthritis, or lupus. The present sequence is that of the A box of human HMGB1. An identical sequence is also found in rat and mouse HMGB1.
 ö
 Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma; inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis; appendicitis; peptic ulcer; duodenal ulcer; crohn's disease; meningitis; allery; immune complex disease; sinusitis; bronchitis; atherosclerosis; emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis; Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes; Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease; amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis; gene, therapy; human immunodeficiency virus; HMGBI protein; mutant;
 invention provides antibodies, or their antigen-binding fragments,
 Gapa
 New isolated polypeptide having a vertebrate HMG A box, useful for
 ö
 Length 74;
 Indels
 100.0%; Score 110; DB 9; 100.0%; Pred. No. 8.9e-09;
 0; Mismatches
 (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES. (GEHO) GEN HOSPITAL CORP. (UYPI-) UNIV PITTSBURGH.
 Ä.
 Fink
 AAE35867 standard; protein; 182 AA
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Yang H, Warren HS,
 Human HMG1 protein mutant #1.
 15-MAY-2002; 2002WO-US015329
 15-MAY-2001; 2001US-0291034P
 Query Match
Best Local Similarity 100.0
 17-JUN-2003 (first entry)
 WPI; 2003-120594/11.
 Sequence 74 AA;
 WO200292004-A2.
 Homo sapiens.
 21-NOV-2002
 racey KJ,
 Synthetic.
 mutein.
 RESULT 13
 AAE35867
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The invention relates to high mobility group (HMG) protein comprising DNA binding motifs termed HMG A box and HMG B box. HMG A box or a nonnaturally occurring HMG A box inhibits the release of a pro-inflammatory cytokine from a vertebrate cell. The methods and compositions of the invention are useful for inhibiting a condition characterised by activation of an inflammatory cytokine cascade such as endotoxic shock, rheumatory cytokine cascade such as endotoxic shock, rheumatorid arthritis, appendictis, peptic or duodenal ulcers, Crohn's disease, peritonitis, hepatitis, asthma, allergy, immune complex disease, sinusitis, bronchitis, emphysema, HIV infection, candidisais, malaria, filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease, myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout, cerebral infarction, neuritis, Goodpastures syndrome, graft-versus-host disease, diabetes and Hodgkin's disease. The invention is useful in gene therapy. The present sequence is human HMG1 (also termed as HMGB1)
inhibiting a condition associated with an activated inflammatory cytokine cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV infection, malaria and diabetes.
 Example 1; Page 37; 82pp; English.
 therapy. The present sequence is
protein (carboxy terminus) mutant
```

Sequence 182 AA;

```
Length 182;
 Indels
100.0%; Score 110; DB 6;
100.0%; Pred. No. 2.1e-08;
iive 0; Mismatches 0;
 1 FKDPNAPKRLPSAFFLFCSE 20
 20; Conservative
 Local Similarity
 83
 Query Match
 Matches
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 8
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Gaps

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RESULT 14

AD025936 standard; protein; 182 AA. AD02593 

AD025936;

(first entry) 26-AUG-2004

Human high mobility group box 1 C-terminal mutant.

cytostatic; gene therapy; vaccine; pharmaceutical composition; HMGB B box; high mobility group; immune response; immunostimulation; cancer; human; high mobility group box 1; HMG1; cytokine activity; mutant; mutein.

Homo sapiens.

Synthetic.

WO2004046338-A2

03-JUN-2004

19-NOV-2003; 2003WO-US036975.

20-NOV-2002; 2002US-0427848P

(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

Tracey KJ

WPI; 2004-420625/39

New pharmaceutical composition comprises a polypeptide comprising an HMGB B box or its functional variant, useful for stimulating or increasing an immune response in an individual or for treating cancer in an individual.

Example 1; SEQ ID NO 19; 68pp; English.

The invention describes a pharmaceutical composition comprising a polypeptide comprising an HMGB (high mobility group box) B box or its

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 The invention relates to a polypeptide comprising a high mobility group box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of a proinflammatory cytokine from a cell treated with an HMGB protein. The invention also relates to a purified preparation of antibodies that specifically bind to the HMGB B box but do not specifically bind to one box epitopes of HMGB, where the antibodies can inhibit release of a proinflammatory cytokine from a cell treated with HMGB, a method for
 Human; high mobility group box 1, HMGB1, HMGB, HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation; inflammatory cytokine cascade; sepsis; allograft rejection; rheumatord arthritis; aschma, lupus; adult respiratory distress syndrome; chronic obstructive pulmonary disease; psoriasis; pancreatitis; peritonitis; burn; myocardial ischaemia; organic ischaemia; reperfusion ischaemia; Behcet's disease; graft-versus-host disease; Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
 New high mobility group box proteins, useful in treating obesity, sepsis, rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia, Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
functional variant to treat a disease or condition by increasing an immune response in an individual administered with the pharmaceutical composition. Also described are: an antibody attached to a polypeptide comprising an HWGB B box or its functional variant; stimulating or increasing an immune response in an individual in need of immunostimulation; and treating cancer in an individual. The composition is useful for stimulating or increasing an immune response in an individual in need of immunostimulation or for treating cancer in an individual. This is the amino acid sequence of a human high mobility group box 1 (HMGI) C-terminal mutant.
 Gaps
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 Length 182;
 Human high mobility group box 1 (HMGB1) mutant protein #1.
 Indels
 ; Score 110; DB 8;
; Pred. No. 2.1e-08;
0; Mismatches 0;
 Example 1; SEQ ID NO 19; 113pp; English.
 Ä
 (CRIT-) CRITICAL THERAPEUTICS INC.
 89 FKDPNAPKRLPSAFFLFCSE 108
 20
 ADO71495 standard; protein; 182
 100.0%;
 1 FKDPNAPKRLPSAFFLFCSE
 20-NOV-2003; 2003WO-US037507.
 20-NOV-2002; 2002US-0427841P
 20-NOV-2002; 2002US-0427846P
 Ouery Match
Best Local Similarity 100....
 (first entry)
 Newman W, O'keefe TL;
 WPI; 2004-420628/39.
 Sequence 182 AA;
 WO2004046345-A2.
 mutant; mutein.
 sapiens.
 26-AUG-2004
 03-JUN-2004.
 Synthetic.
 AD071495;
 RESULT 15
 AD071495
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CC determining whether a compound inhibits inflammation, a method of determining whether a compound inhibits inflammation, a pharmaceutical composition comprising an HWGB protein or an antibody that binds to the protein, an agent that inhibits TMP biological activity and a method of treating a condition in a patient characterised by activation of an circular acts of the patient comprises administering weight loss or treating obesity in a patient comprises administering to the patient amount of the colypeptide. The polypeptide, antibodies, composition and methods are cuseful in treating obesity and conditions characterised by activation of an inflammatory cytokine cascade, e.g. sepsis, allograft rejection, continuation arthritis, asthma, lupus, adult respiratory distress syndrome, chronic obstructive pulmonary disease, psoriasis, pancreatitis, chronic obstructive pulmonary disease, psoriasis, pancreatitis, continuis, burns, myocardal schaemia, organic ischaemia, reperfusion cischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease, cronic coltis, multiple sclerosis or cachexia. This sequence continuant models mutant polypeptide of the invention.
```

Query Match 100.0%; Score 110; DB 8; Length 182; Best Local Similarity 100.0%; Pred. No. 2.1e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Search completed: April 6, 2006, 10:19:09 Job time : 25.2763 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
```

OM protein - protein search, using sw model

Run on:

(without alignments) 504.309 Million cell updates/sec 6, 2006, 10:19:38 ; Search time 3.81579 Seconds April

US-10-717-984-23 Perfect score:

1 FKDPNAPKRLPSAFFLFCSE 20 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Clacession: A27853
Rilee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A; Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA sp. A; Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA sp. A; Reference number: A27853, MUID:87259966; PMID:3601666
A; Accession: A27853
A; Residues: 1-170 cLEE>
A; Residues: 1-170 cLEE>
A; Residues: 1-170 cLEE>
C; Superfeatly: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
F; 1-38/Domain: HMG box homology (fragment) cHMG1>
F; 47-121/Domain: HMG box homology cHMG2>

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Gaps

Query Match 93.6%; Score 103; DB 2; Length 170; Best Local Similarity 95.0%; Pred. No. 6.6e-09; Matches 19; Conservative 0; Mismatches 1; Indels 0;

| high mobility grouhigh mobility grou | high mobility grou | high mobility grou | HMG protein (impor | high mobility grou | probable HMG prote | high mobility grou | high mobility grou | high mobility grou | HMG protein 1.1 - | hypothetical prote | HMG1 protein - sea | nonhistone chromos | high mobility grou |        |
|--------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|
| T03375                               | T02252             | \$22309            | T51159             | 839556             | F84553             | T51596             | \$40302            | S40122             | T43006            | T27004             | JC4357             | A35072             | T04662             | T51598 |
| 0,0                                  | ı N                | 7                  | ~                  | 7                  | ď                  | 7                  | 7                  | ~                  | ~                 | ~                  | 0                  | ~                  | ~                  | ~      |
| 126                                  | 142                | 152                | 178                | 149                | 138                | 138                | 144                | 154                | 95                | 312                | 200                | 93                 | 125                | 141    |
| 68.2                                 | 68.2               | 68.2               | 67.3               | 66.4               | 65.5               | 65.5               | 65.5               | 65.5               | 6.09              | 6.09               | 0.09               | 58.2               | 58.2               | 58.2   |
| 75                                   | 75                 | 75                 | 74                 | 73                 | 72                 | 72                 | 72                 | 72                 | 67                | 67                 | 99                 | 64                 | 64                 | 64     |
| 30                                   | 35                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                 | 42                 | 43                 | 44                 | 45     |

## ALIGNMENTS

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Cipacesion: 229857
Ristros, M.; Dixon, G.H.
Biochim: Blophys. Acta 1172, 231-235, 1993
Ristros, M.; Dixon, G.H.
Biochim: Blophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857, MUID:93176821; PMID:8439568
A;Recession: S29857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:9184250; PIDN:AAA64970.1; PII
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Reywords: chromosomal protein Protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
 ö
 A27853
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
 Gaps
 ö
 Length 216;
 Indels
 Query Match 100.0%; Score 110; DB 2; Best Local Similarity 100.0%; Pred. No. 6.5e-10; Matches 20; Conservative 0; Mismatches 0;
nonhistone chromosomal protein HMG-1 - human
 1 FKDPNAPKRLPSAFFLFCSE 20
 83
 RESULT 2
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A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:CA:R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
ERSE Lett. 122, 254-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
 A;Molecule type: protein
A;Rosidues: 2.22, %.24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Rosidues: 2.22, %.24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FRBS Lett. 267, 139-141, 1990
A;Fitle: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-c.A;Reference number: S10726; MUID:90306387; PMID:2365081
 A/Accession: S10959
A/Molecule type: protein
A/Residues: 2-22, "x',24-38 cCHR>
A/Cross-references: UNIPARC:UPI0000173989
R/Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1384
A/Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group A/Reference number: 145910, MUID:84128872; PMID:6141822
A/Accession: 145910
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Ross-references: UNIPARC:UPI00016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:çKeywords: chromosomal protein HMG-2; HMG box homology
C/Superfamily: nonhistone chromosomal protein HMG-1 #status predicted cMAT>
 A;Accession: $02826
A;Molecule type: mRNA
A;Residues: 1-215 <MENA
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Blectrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot
A;Reference number: A33178; MUID:91176935; PMID:2079031
 R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
 A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
 C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
 Gaps
 ö
 Length 215;
 Indels
 93.6%; Score 103; DB 1; Lv 95.0%; Pred. No. 8.3e-09; live 0; Mismatches 1;
 nonhistone chromosomal protein HMG-1 - human
C; Accession: S01947; A61611; S10959; 145910
 A,Molecule type: protein
A,Residues: 2-13, XXF' <WAR>
A;Cross-references: UNIPARC:UP100001771D7
A;Accession: G33178
 F;92-166/Domain: HMG box homology <HMG2>
 89 FKDPNAPKRPPSAFFLFCSE 108
 6-83/Domain: HMG box homology <HMG1>
 1 FKDPNAPKRLPSAFFLFCSE 20
 R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence
 Query Match
Best Local Similarity 95.0
Matches 19; Conservative
 A, Molecule type: protein
 A; Molecule type: mRNA
A; Residues: 1-215 <KAP>
 A; Accession: S01947
 A;Accession: A61611
 A; Accession: A33178
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 RESULT 3

NARTHI

NONDISCORDED STATE OF THE
 A; Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-termina
 A.Molecule type: protein
A.Molecule type: protein
A.Residues: 98-105, XX. 107-112 <PA2>
A.Residues: 98-105, XX. 107-112 <PA2>
A.Cross-references: UNIPARC. UPIDO00017396
A.Residues source: postnatal brain
A.Note: sequence extracted from NCBI backbone (NCBIP:137788)
C.Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C.Superfamily: nonhistone chromosomal protein; NNA binding; nucleus
C.Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAI>
 ö
 RESULT 4
S01947
nonhistone chromosomal protein HMG-1 - bovine
NyAlternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
 Gaps
 Query Match 93.6%; Score 103, DB 1; Length 215; Best Local Similarity 95.0%; Pred. No. 8.3e-09; Matches 19; Conservative 0; Mismatches 1; Indels
 F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
 89 FKDPNAPKRPPSAFFLFCSE 108
 FKDPNAPKRPPSAFFLFCSE 63
 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
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A;Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PID: A;Note: the authors did not translate the codon for residue 1
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>
 C;Accession: S30221
R;Alexandre, S.; Li, W.W.; Lee, A.S.
Nucleic Acids Res. 20, 6413, 1992
Nucleic Acids Res. 20, 6413, 1992
Nucleic Acids Res. 20, 6413, 1992
A;Title: A human HWG2 CDNA with a novel 3'-untranslated region.
A;Reference number: S30221; MUID:93117123; PMID:1475204
A;Accession: S30221
A;Accession: S30221
A;Accession: 1-186 AcMLE>
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: 1-186 AcMLE>
A;Residues: 1-186 AcMLE>
A;Cross-references: UNIPROT:P26583; UNIPARC:UP1000016AA6C; EMBL:Z17240; NID:g32334; PIDN
A;Cross-references: UNIPROT:P26583; UNIPARC:UP1000016AA6C; EMBL:Z17240; NID:g32334; PIDN
A;Cross-references: Uniparcy october 1992
C;Superfamily: nonhistone chromosomal protein HWG-2; HMG box homology
 mouse Hn
 A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-215 (RE2>
A,Cross-references: UNIPARC:UP100000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PII
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 linker histones B4 and
 A; Title: Molecular cloning, expression analysis, and chromosomal localization of A; Reference number: 157021; MUID:94235965; PMID:8180479
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 high mobility group protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62355
 C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
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 Length 215;
 90.9%; Score 100; DB 2; Length 210; 90.0%; Pred. No. 2.4e-08;
 and
 Rivightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P. EMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 as A;Reference number: S62355; MUID:96174815; PMID:859938
A;Accession: S62355
A;Status: preliminary, nucleic acid sequence not shown A;Residues: 1-210 <NIG>
 nonhistone chromosomal protein HMG-2B - human (fragment)
 Query Match
93.6%; Score 103; DB 2;
Best Local Similarity 95.0%; Pred. No. 8.3e-09;
Matches 19; Conservative 0; Mismatches 1.
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 1; Mismatches
 C; Kerwords: chromosomal protein
F;6-81/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
 89 FKDPNAPKRPPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Local Similarity 90.0 les 18; Conservative
 A; Accession: I57021
 Query Match
 A;Gene: hmg1
 C, Genetics:
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 non-histone chromosomal high-mobility group 1 protein - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 148688; A55402; E7021
R; Yotov, W.V.; St.-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A; Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mc A; Reference number: 148687; MUD: 92335012; PMID: 1630928
A; Reference number: 148688
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-215 < RES
A; Cross-references: UNIPROT: P07155; UNIPARC: UPI00000008A6; EMBL: Z11997; NID: 953381; PIDN
B; Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J; Biol. Chem. 269, 28803-28808; 1994
A; Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A; Reference number: A55402; MUD: 95050689; PMID: 7961836
A; A; Accession: A55402; MUD: 95050689; PMID: 7961836
 RESULT 6

ADA8897

Nonhistone chromosomal protein HMG-1 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: A28897

E;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.

Biochemistry 27, 6159-6163, 1988

A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequent A28897.

A;Accession: A28897.
 A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-215 < rgCu.
A; Residues: 1-215 < rgCu.
A; Cross-references: UNIPROT: P12682; UNIPARC: UPI000016C6C4; GB: M21683; GB: M21684; NID: 916
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Keywords: chromosomal protein; DNA binding; nucleus
F; 6-84) Domain: HMG box homology < HMG1.>
F; 992-166/Domain: HMG box homology < HMG2.>
 A,Cross-references: UNIPARC:UP100016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
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A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UP100001771D7
C;Genetics:
A;Genetics:
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
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F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>
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 93.6%; Score 103; DB 2; Length 215; 95.0%; Pred. No. 8.3e-09; ive 0; Mismatches 1; Indel8
 Length 215;
 A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
 1; Indels
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FKDPNAPKRPPSAFFLFCSE 108
 89 FKDPNAPKRPPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 Best Local Similarity 95.0
Matches 19; Conservative
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1; Indels

Score 97; DB 2; 1 Pred. No. 6.4e-08;

88.2%; milarity 94.7%; Conservative 0

Query Match Best Local Similarity Matches 18; Conserv

0; Mismatches

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A; Molecule type: DNA
A; Residues: 2-209 <SHI>A; Residues: 2-209 <SHI>A; Cross-references unippror: D26583; UNIPARC: UPI000012CA25; GB: M83665; NID: 9184235; PIDN: IA; Note: initiator Met not shown
B; Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M; Tile: Sequence of human HMG2 cDNA.
A; Tile: Sequence of human HMG2 cDNA.
A; Reference number: S20061; MUID: 92093633; PMID: 1754403
 nonhistone chromosomal protein HMG-2 - pig
C,Species: Sus scrofa domestica (domestic pig)
C,Species: Sus scrofa domestica (domestic pig)
C,Bate: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C,Accession: A34719
R,Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A,Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nuclec
A,Reference number: A34719; MUID:90275208; PMID:2350545
 A Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:J
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Reywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
 A; Cross-references: UNIPARC: UP1000013E34D; EMBL: X62534; NID: 932332; PIDN: CAA44395.1; PID
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 high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Daceies: Cot-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S; Koenig, H:; Wirth, T.
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 A Gene: GDB:NHCP2
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
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 Length 209;
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Pred. No. 7.2e-08;
0; Mismatches 1; Indels
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 R;Shirakawa, H.; Yoshida, M.
Calol. Chem. 267, 6641-6645, 1992
A;Title: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
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88.2%; Score 97; DB 1; 1

Best Local Similarity 94.7%; Pred. No. 7.2e-08;

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 2 KDPNAPKRLPSAFFLFCSE 20
 2 KDPNAPKRLPSAFFLFCSE 20
C; Accession: A42425; S20061; S18068
 Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative (
 A; Molecule type: mRNA
A; Residues: 1-209 < MAJ>
 A;Status: preliminary
 C, Genetics:
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 nonhistone chromosomal protein HMG-2 - chicken
NoAlternate names: high-mobility-group protein 2
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: O5-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
C.Accession: U51129
R.Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A.Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A.Reference number: JC1129; MUID:92290291; PMID:1601311
A.Recession: JC1129
A.Molecule type: mRNA
A.Residues: 1-207 <SPA>
A.Molecule type: mRNA
A.Residues: 1-207 <SPA>
A.CCOSSION: UNIPROT:P26584; UNIPROT:
 Joil14

Light-mobility group protein 2 - chicken

Light-mobility group protein 2 - chicken

Cispecies: Gallus gallus (chicken)

Cispecies: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Cipate: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Cipate: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

Ribavis, D.L.; Burch, J.B.E.

Gene 113, 251-256, 1992

Aprille: 1801ation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt

Apricession: JC1114; MUID:92241676; PMID:1572546
 A)Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:M81235; NID:g211926; PIDN: C;Comment: The high mobility group proteins are among the most abundant nonhistone chromeoscal protein HMG-2; HMG box homology C;Superfamily: nonhistone chromeoscal protein HMG-2; HMG box homology C;Keywords: DNA binding; nucleus F;6-83/Domain: HMG box homology <HMG1> F;92-166/Domain: HMG box homology <HMG2>
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 Match 88.2%; Score 97; DB 2; Length 207; Local Similarity 94.7%; Pred. No. 7.1e-08; es 18; Conservative 0; Mismatches 1; Indels
 Length 186;
 Length 207;
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90 KDPNAPKRPPSAFFLFCSE 108

RESULT 11

A; Molecule type: mRNA A; Residues: 1-207 < DAV>

2 KDPNAPKRLPSAFFLFCSE 20

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Query Match

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nonhistone chromosomal protein HMG-2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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 90 KDPNAPKRPPSAFFLFCSE 108
 2 KDPNAPKRLPSAFFLFCSE 20
 RESULT 12
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14, 1198-1208, 1995

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RESULT 15
D61510
high mobility group protein 1 - African clawed frog (fragment)
high mobility group protein 1 - African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: D61510
R;Grossberger, D: Falink, M.; Marcuz, A.
Comp. Biochem. Physiol. B 98, 127-133 1991
A;Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated
A;Reference number: A61510; MUID:91284580; PMID:2060276
A;Reference number: A61510; MUID:91284580; PMID:2060276
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-49 <GRO>
A;Cross-references: UNIPARC:UPI00001771D3
C;Superfamily: nonhistone chromosomal protein HWG-2; HWG box homology
A.Title: High mobility group protein 2 functionally interacts with the POU domains of of A, Reference number: S54774, MUID:95237201; PMID:7720710
A, Accession: S54774
A, Status: preliminary; nucleic acid sequence not shown
A, Status: preliminary; nucleic acid sequence not shown
A, Residues: 1-210 < ZMIA
A, Residues: 1-210 < ZMIA
A, FORSE-references: UNIPROT:P30681; UNIPARC:UP1000016432C; EMBL:246757; NID:g609168; PIL
C, Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F, 6-83/Domain: HMG box homology < HMG1>
F, 92-166/Domain: HMG box homology < HMG2>
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 Query Match 88.2%; Score 97; DB 2; Length 210; Best Local Similarity 94.7%; Pred. No. 7.2e-08; Matches 18; Conservative 0; Mismatches 1; Indels
 90 KDPNAPKRPPSAFFLFCSE 108
 2 KDPNAPKRLPSAFFLFCSE 20
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Query Match 86.4%; Score 95; DB 2; Length 49; Best Local Similarity 89.5%; Pred. No. 3.5e-08; Matches 17; Conservative 1; Mismatches 1; Indels

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Search completed: April 6, 2006, 10:26:17 Job time : 3.81579 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

6, 2006, 10:13:48; Search time 23.6184 Seconds April Run on:

(without alignments) 597.439 Million cell updates/sec

US-10-717-984-23

110 1 FKDPNAPKRLPSAFFLFCSE 20 score: Perfect

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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|           | g                     | mischill      |        | ambystoma    |              |              |              |              |              | mus musculu  | cricetulus | musculu       | o sapien | mus musculu | homo sapien | xenopus tro | xenopus lae  | bos taurus | canis famil | homo sapien | mus musculu | sus scrofa | rattus norv | gallus gall  | ũ       |        | macaca fasc |        | spalax leuc | spalax leuc  |          | rattus norv |
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|           | Description           | OBbd02        | 080vz1 | 090228       | Q5t7c1       | Q5t7c2       | Q5t7c4       | Q5t7c6       | Q59gw1       | Q8c7c4       | P07156     | Q8bnm0        | Q5t7c5   | QSbkq1      | 09nqj 4     | Q6p4n5      | Q78242       | P10103     | Q6yka4      | P09429      | P63158      | P12682     | P63159      | O9puk9       | 014321  | Q5t7c3 | Q4r844      | 088611 | 088612      | 09qwy6       | 094x40   | Q548r9      |
|           |                       |               |        |              |              |              |              |              |              |              |            |               |          |             |             |             |              |            |             |             |             |            |             |              |         |        |             |        |             |              |          |             |
| SUMMARIES |                       | DAROD2 MOTTSE | MOUSE  | Q90228 AMBME | QST7C1 HUMAN | QST7C2_HUMAN | QST7C4_HUMAN | QST7C6_HUMAN | Q59GW1_HUMAN | Q8C7C4_MOUSE | RIGR       | DABNIMO MOUSE |          |             | HUMAN       | XENTR       | Q7SZ42_XENLA | NIVO       | ANFA        | IUMAN       | IOUSE       | JIG.       | 'AT         | Q9PUK9_CHICK | 1 HUMAN | HUMAN  |             | SPAEH  | 2_SPAEH     | Q9QWY6_SPAEH | SPAEH    | RAT         |
| SOS       | ΩI                    | OBBODS        | 080YZ1 | 090228       | Q5T7C1       | Q5T7C2       | Q5T7C4       | Q5T7C6       | Q59GW1       | Q8C7C4       | HMG1_CRIGR | Q8BNM0        | Q5T7C5   | Q5BKQ1      | 09NQJ4      | Q6P4N5      | Q7SZ42       | HMG1_B     | HMG1_CANFA  | HMG1_HUMAN  | HMG1 N      | HMG1 P     | HMG1_RAT    | Q9PUK9       | 014321  | Q5T7C3 | Q4R844      | 088611 | 088612      | O9QWY6       | Q9QX40   | 0548R9      |
|           | DB                    |               | 1 (1   | ~            | N            | N            | 7            | 7            | ~            | ~            | ٦          | ~             | ~        | ~           | ~           | N           | 7            | 1          |             | 1           | 7           | ч          | -           | N            | ~       | 7      | ~           | ~      | N           | ~            | 7        | ~           |
|           | Query<br>Match Length | 215           | 208    | 216          | 132          | 157          | 158          | 162          | 176          | 178          | 180        | 181           | 192      | 206         | 211         | 211         | 211          | 214        | 214         | 214         | 214         | 214        | 214         | 214          | 215     | 215    | 215         | 215    | 215         | 215          | 215      | 215         |
| d         | Query<br>Match        | 100.0         | 94.5   |              | •            | 93.6         | ë.           | 93.6         | ë.           |              | 93.6       | 93.6          | 93.6     | 93.6        | <u>.</u>    | θ,          | θ.           | ë          | ë.          | 93.6        | 93.6        | Э,         | ٠           | 93.6         | 93.6    | ω.     | •           | ن      | ش           | 93.6         | 93.6     | 93.6        |
|           | Score                 | 110           | 104    | 104          | 103          | 103          | 103          | 103          | 103          | 103          | 103        | 103           | 103      | 103         | 103         | 103         | 103          | 103        | 103         | 103         | 103         | 103        | 103         | 103          | 103     | 103    | 103         | 103    | 103         | 103          | 103      | 103         |
|           | Result<br>No.         |               | 1 0    | m            | 4            | Ŋ            | 9            | 7            | 80           | 6            | 10         | 11            | 12       | 13          | 14          | 15          | 16           | 17         | 18          | 19          | 50          | 21         | 22          | 23           | 24      | 25     | 56          | 27     | 28          | 53           | 30       | 31          |

NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

| Q58evS m high mobi<br>Q9yh06 gallus gall<br>Q6nx86 brachydanio<br>Q7zvc6 brachydanio<br>Q4rrhy tetraodon n<br>Q91596 xenopus lae<br>Q6mq5 xenopus lae<br>Q9uq5 homo sapien<br>Q9ct19 mus musculu<br>Q9ct19 mus musculu<br>Q9ct35 pagrus majo<br>P40618 gallus gall<br>P26584 gallus gall |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 058EV5_MOUSE<br>09YH06_CHICK<br>06NX86_BRARE<br>047XV66_BRARE<br>041596_XENLA<br>091596_XENLA<br>HMG1X_HUMAN<br>09CT19_MOUSE<br>096753_HUMAN<br>09CT19_MOUSE<br>096735_PAGMA<br>HMG2_CHICK<br>HMG2_CHICK                                                                                 |
| 000000000000                                                                                                                                                                                                                                                                             |
| 215<br>2015<br>2015<br>2005<br>2010<br>2010<br>1995<br>2001<br>2006                                                                                                                                                                                                                      |
| 88888880000000000000000000000000000000                                                                                                                                                                                                                                                   |
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## ALIGNMENTS

Arakawa T., Shinagawa A., Shibata K., Yoohino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsudo T., Gasterland T., Gissi C., King B., Kochiwa H., Ratsuo Y., Matsuo J., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazhara I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mayashizaki Y., Kawaji H., Kohtsuki S., Hasegawa Y., Kawaji H., Kohtsuki S., STRAIN=CS7BL/6J; TISSUE-Spinal ganglion;
MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999). 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130095009 product:high mobility group box 1, Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). NUCLECTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Spinal ganglion; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; 215 AA. PRT; QBEO02\_MOUSE

OBEO02\_MOUSE

O OBEO02\_MOUSE PRELIMINARY;

AC OBEO02\_DI (TERMBLEE]. 23,

DT 01-MAR-2003 (TERMBLEE]. 26,

DE MUS musculus 12 days embryo

DE full insert sequence.

GN Name=HmQb;

OS Mus musculus (Mouse).

OC Muridae; Murinae; Mus.

OC Muridae; Murinae; Mus.

OC MURIT TAXID=10090;

RN NUCLEOTIDE SEQUENCE.

STRAIN=C75BL/61; TISSUE=Spin

RN MUCLEOTIDE SEQUENCE.

RY MEDLINE=99279253; PubMed=112

RN WEDLINE=99279253; PubMed=112

RN WEDLINE=2016666; PubMed=112

RA Arawawa T., Hara A., Fukunis

RA Arawawa T., Shinagawa A., Shil

RA Sakai K., Okido T., Furuno P

RA Bake J., Boffelli D., Bojuu

RA Hayashizaki Y.,

RY HAYASHIS GONOI).

RY HAYASHIS GONOID.

RY HARINGSTBL/GO; TISSUE=Spin

RY HARINGSTBL/GO; TISSUE=S

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Charlemagne J.;
"High levels of HMG1-2 protein expression in the cytoplasm and nucleus
"High levels of HMG1-2 protein expression in the cytoplasm and nucleus
hydrocortisone sensitive amphibian thymocytes.";
Biol. Cell 69:153-160(1990).
EMBL; U31513; AAB08831.1; -; mRNA.
 A Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
Botcherby M.R.M.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; ALG/0999; CADB3017.1; -; Genomic_DNA.

R SMR; G00725; 1NRN.

R SMR; G00725; 1NRN.

R SMR; G00725; 1NRN.

R G0; G0.0000785; C:chromatin; IEA.

G0; G0.0000785; C:chromatin; IEA.

G0; G0.0006357; F:DNA binding; IEA.

G0; G0.0006357; F:DNA binding; IEA.

R G0; G0.0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000135; Highmoblty_12.

R InterPro; IPR00195; Highmoblty_12.

R PRINTS; PR00886; HIGHMOBLTY12.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBL_TaxID=10090;
 MEDLINE-56263706; PubMed-8654668; DOI=10.1016/0145-305X(95)00025-0; de Guerra A., Guillet F., Charlemagne J., Fellah J.S.; "Identification of CoNA clones encoding HMG 2, a major protein of the mexican axolotl hydrocortisone-sensitive thymocytes."; Dev. Comp. Immunol. 19:417-423(1995).
 PubMed=2097001;
Guillet F., Tournefier A., Denoulet P., Capony J.P., Kerfourn F.,
Charlemagne J.;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BM168F16.1 (Novel protein similar to high-mobility group box 1
 North P., Leaves N., Greystrong J., Coppola M., Manjunath S.,
Russell E., Smith M., Strachan G., Tofts C., Boal E., Cobley V
Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
 4DBCB7B9516D7B52 CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 94.5%; Score 104; DB 2; Le
95.0%; Pred. No. 1.88-08;
Mismatches 1;
 216 AA
 High mobility group protein-2 (HMG-2)
 PRT;
 89 FKDPNAPKRSPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
 Ambystoma mexicanum (Axolot1).
 208 AA; 23811 MW;
 Q90228 AMBME PRELIMINARY;
Q90228;
 19; Conservative
 SM00398; HMG; 2.
 Name=bM168F16.1;
Mus musculus (Mouse).
 NUCLEOTIDE SEQUENCE.
 NUCLEOTIDE SEQUENCE.
 Best Local Similarity
 PROTEIN SEQUENCE.
 NCBI_TaxID=8296;
 SEQUENCE
 Query Match
 AMBME
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 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu M., Hiraoka T., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Arach H., Kawai J., Kojima Y., Konno B., Konno H., Kona M., Nakamura T., Misazaki Y., Konno M., Ohsaro N., Okazaki Y., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsaro N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazu N., Okazaki Y., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Yagami M., Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Millian Shi M., S
 NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUB=Spinal ganglion;
MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 Gaps
 MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamancto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabliwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Tozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riksi integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
 ö
 100.0%; Score 110; DB 2; Length 215; 100.0%; Pred. No. 2e-09; ive 0; Mismatches 0; Indels (
 8A86969266DC07F5 CRC64;
 Created)
Last sequence update)
 208 AA
 PRT;
 InterPro; IPR000135; Highmoblty_12.
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 2.
 FKDPNAPKRLPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
 PRINTS; PR00886; HIGHMOBLTY12.
 215 AA; 24905 MW;
 080YZ1
Q80YZ1,
01-JUN-2003 (TEMBLrel. 24,
01-JUN-2003 (TEMBLrel. 24,
 20; Conservative
 Nature 420:563-573(2002)
 SMART; SM00398; HMG; 2.
 NUCLEOTIDE SEQUENCE
 NUCLEOTIDE SEQUENCE
 Best Local Similarity
 SECUENCE
 Query Match
 MOUSE
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Matches

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RESULT 2
QBOYZ1 MO
ID QBOY
AC QBOY
DT 01-J

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Gaps

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Length 208;

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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-mobility group box 1 (Fragment).
Name-HWGB1; OrNames-RP11-550P23.1-009;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 EMBL; AL353648; CAL15604.1; -; Genomic_DNA.

SMR; Q5T7C2; 2-84, 89-157.

GO; GO:000785; C:chromatin; IEA.

GO; GO:0005631; C:mucleus; IEA.

GO; GO:0003577; F:DNA binding; IEA.

GO; GO:0003577; F:DNA binding; IEA.

InterPro; IPR000135; Highmoblty_12.

InterPro; IPR000105; HMG box; Z.

PFINITS; PR0086; HJGHWOBLTY12.
 Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, AL353648; CAI15603.1; -; Genomic_DNA.

EMBL, AL353648; CAIL5603.1; -; Genomic_DNA.

EMBL, OSTOCH, 2-84, 89-157.

GO; GO:0000785; C:chromatin; IEA.

GO; GO:00005634; C:uncleus; IEA.

GO; GO:0003577; F:DNA binding; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000910; Highmoblty_12.

InterPro; IPR000910; HMG 12 box.

Pfam; PF00505; HMG box; Z.
 93.6%; Score 103; DB 2; Length 157; 95.0%; Pred. No. 2e-08; 1; Indels 1; Indels
 93.6%; Score 103; DB 2; Length 158; 95.0%; Pred. No. 2e-08;
 Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 157 157
157 AA; 18164 MW; F38343E7F52FC457 CRC64;
 PROSITE; PS00353; HMG BOX 1; 1.
PROSITE; PS50118; HMG BOX 2; 2.
SEQUENCE 158 AA; 18311 MW; 1A438343E7F52FC4 CRC64;
 Ol-FBB-2005 (TrEMBLrel. 29, Created)
01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
High-moblity group box 1.
Name-HMGB1; ORFNames=RP11-550P23.1-003;
 FKDPNAPKRPPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG_BOX_1; 1.
PROSITE; PS50118; HMG_BOX_2; 2.
 PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
 QST7C4_HUMAN PRELIMINARY;
 Query Match
Best Local Similarity 95.0
Matches 19; Conservative
 NUCLEOTIDE SEQUENCE.
 Homo sapiens (Human)
 NUCLEOTIDE SEQUENCE.
 Best Local Similarity
 Homo.
NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 NON TER
SEQUENCE
 Pelan S.;
 SEQUENCE
 Query Match
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PIR, A60975; A60975.

R SNR, P00125; LCKT.

R SNR, Q90228; 2-84, 90-167.

R CO; GO:0000785; C:chromatin; IEA.

R CO; GO:0005634; C:nucleus; IEA.

R CO; GO:000557; F:DNA binding; IEA.

R CO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000315; HNG 12_box.

R INTERP: PR000315; HNG 12_box.

P Fam; PR00505; HNG box; 2.

PRINTS; PR00886; HIGHMOBLTY12.

R SNART; SM00398; HNG 3.

PROSITE; PS00135; HMG Box 1: 1.

PROSITE; PS00135; HMG Box 2: 2.

R PROSITE; PS00135; HMG Box 2: 2.

R PROSITE; PS00135; HMG Box 2: 2.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 GO; GO: 0000785; C: chromatin; IEA.
GO; GO: 0005634; C: nucleus; IEA.
GO; GO: 0005634; C: nucleus; IEA.
GO; GO: 0005675; P: DA binding; IEA.
GO; GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000135; Highmoblty_12.
InterPro; IPR00910; HWG 12_box.
PRINTS; PR00886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
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 93.6%; Score 103; DB 2; Length 132; 95.0%; Pred. No. 1.7e-08; ive 0; Mismatches 1; Indels
 94.5%; Score 104; DB 2; Length 216; 100.0%; Pred. No. 1.9e-08; ive 0; Mismatches 0; Indels
 Pelan S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 132 AA; 15185 MW; COFAC527E53F9356 CRC64;
 01-FEE-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
High-moblity group box 1 (Fragment).
Name-HWGB1; ORFNames-RP11-550P23.1-006;
 157 AA.
 PRT; 132 AA.
 EMBL; AL353648; CAI15605.1; -; Genomic_DNA
SMR; QST7C1; 2-84.
 Q5T7C2 HUMAN PRELIMINARY; PRT; Q5T7C2; 01-FEB-2005 (TrEMBLrel. 29, Created)
 91 KDPNAPKRLPSAFFLFCSE 109
 1 FKDPNAPKRLPSAFFLFCSE 20
 2 KDPNAPKRLPSAFFLFCSE 20
 PROSITE; PS00353; HMG BOX 1; 1. PROSITE; PS50118; HMG BOX 2; 2. NON TER 132 132
 Query Match
Best Local Similarity 100.C
 QST7C1 HUMAN PRELIMINARY;
QST7C1;
 19; Conservative
 Homo sapiens (Human)
 Best Local Similarity
 NUCLEOTIDE SEQUENCE.
 NCBI_TaxID=9606;
 SEQÜENCE
 Query Match
 HUMAN
 HUMAN
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Matches

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Gaps

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NUCLEOTIDE SEOUENCE
 NUCLEOTIDE SEOUENCE.
 NUCLEOTIDE SEQUENCE
 NUCLEOTIDE SEQUENCE
 Query Match
Best Local Similarity
Matches 19; Conserv
 NCBI_TaxID=10090,
 Hayashizaki Y.;
 Name=Hmgb1;
 MOUSE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
 Gaps
 Gaps
 TISSUE-Myeloblast cell line;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S., Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
 ö
 ö
 Length 162;
 Score 103; DB 2; Length 16
Pred. No. 2.1e-08;
0; Mismatches 1; Indels
1; Indels
 Pelan S.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 "None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
 176 AA; 20164 MW; C31A7039D92649D9 CRC64;
 10-MAY-2005 (TrEWBLrel. 30, Last sequence update)
High-mobility group box 1 variant (Fragment).
Bukarvara saplens (Human).
 01-FEB-2005 (TrEMBLrel. 29, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 162 AA.
 176 AA.
 EMBL; AL353648; CAI15601.1; -; Genomic_DNA.
0; Mismatches
 High-mobility group box 1 (Fragment).
Name-HMGB1; ORFNames-RP11-550P23.1-002;
Homo sapiens (Human).
 Created)
 PRT;
 EMBL, AB208998; BAD92235.1; -; mRNA.
NON TER 1
SEQÜENCE 176 AA; 20164 MW; C31A'
 FKDPNAPKRPPSAFFLFCSE 108
 FKDPNAPKRPPSAFFLFCSE 108
 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 93.6%;
 01-FEB-2005 (TrEMBLrel. 29,
 10-MAY-2005 (TrEMBLrel. 30,
 Ouery Match
Best Local Similarity 95.v.,
Conservative
 QST7C6_HUMAN PRELIMINARY;
 Q59GW1 HUMAN PRELIMINARY;
O59GW1;
19; Conservative
 NUCLEOTIDE SEQUENCE
 NUCLEOTIDE SEQUENCE
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 HUMAN
 HUMAN
 Matches
 Homo.
 RESULT 8
(05964) 1 HU
(05944) 1 HU
(05944) 1 HU
(0594) 1 HO
(0594)
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 Carraines Several Series Serie
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 STRAIN=C57BL/67; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Notazaki Y., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone: C920030E14 product: high mobility group
 TRAIN=CSTBL/66; TISSUE=Thymus;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
 Gaps
 "Functional annotation of a full-length mouse cDNA collection.";
 ö
 Length 176;
Score 103; DB 2; Length 17
Pred. No. 2.2e-08;
0; Mismatches 1; Indels
 178 AA.
 box 1, full insert sequence. (Fragment)
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
 PRT;
 91 FKDPNAPKRPPSAFFLFCSE 110
 1 FKDPNAPKRLPSAFFLFCSE 20
 STRAIN=C57BL/6J; TISSUE=Thymus; The FANTOM Consortium,
 93.6%;
ilarity 95.0%;
Conservative
 Q8C7C4 MOUSE PRELIMINARY;
 Nature 409:685-690(2001).
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NCBI_TaxID=10029;
 Repeat.
DNA_BIND
DNA_BIND
COMPBIAS
NON_TER
HELIX
 SEQUENCE
 removed
 PDB;
PDB;
SMR;
 TURN
 셤
 Adachi J., Alzawa K., Akimura;

RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,

RA Karch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Karch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Karch H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamura M.,

RA Satto R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sagawa D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Sagawi D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RUBLI, AKOSO659; Basasi J., Fakaku-Ashira S., Takada Y., Tanaka T.,

RASP: PO1156; JNHN.

SRR; O8C7C4; 2-84, 93-171.

RO; GO:0005615; C:extracellular space; IDA.

RO; GO:0005615; F:protein binding; IPI.

RO; GO:0006810; P:nitric-oxide synthase regulator activity; IDA.

ROS GO:0006810; P:nitric-oxide synthase regulator.
 ö
 NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUB=Thymus;

MEDLINE=C57BL/6J; TISSUB=Thymus;

MEDLINE=C57BL/6J; TISSUB=Thymus;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Itoh M., Nakamura S., Hazama M., Nishine T., Harada A.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
 (Fragment).
Name=HMGB1; Synonyms=HMG-1, HMG1;
Cricctulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Cricetulus.
 Gaps
 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
High mobility group protein 1 (HMG-1) (High mobility group protein
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 93.6%; Score 103; DB 2; Length 178; 95.0%; Pred. No. 2.3e-08; ive 0; Mismatches 1; Indels
 20303 MW; 155FD80D52960A62 CRC64;
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Pfan; PF00505; HMG box; Z.
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Genome Res. 10:1617-1630(2000)
 19; Conservative
 STANDARD;
 SMART; SM00398; HMG; 2.
 178 AA;
 Local Similarity
 HMG1_CRIGR
P07156;
 NON TER
SEQUENCE
 Query Match
 Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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 MEDLINE=3347974; PubMed=8346022;
Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
"Solution structure of a DNA-binding domain from HMG1.";
Mucleic Acids Res. 21:347-3436 (1933).
-!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
double stranded DNA.
-!- SUBCELLUTAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
-!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
 Gaps
 "Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle expression of the HMC-1 gene."; Overlet Choice Res. 15:5051-5068 (1987).
NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDILINE=8725986; PubMed=3601666;
Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
Dixon G.H.;
 SMART; SM00399; HMG; 2.
PROSITE; PS0033; HMC BOX 1; 1.
PROSITE; PSS0118; HMG BOX 2; 2.
3D-structure; ChromosGmal protein; DNA-binding; Nuclear protein;
 GO; GO:0000793; C:condensed chromosome; ISS.
GO; GO:0008301; F:DNA bending activity; ISS.
GO; GO:000510; F:Drotein binding; ISS.
GO; GO:0005288; P:Dase-excision repair, DNA ligation; ISS.
GO; GO:0006281; P:DNA recombination; ISS.
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GO; GO:0006281; P:DNA unwinding; ISS.
GO; GO:0006282; P:establishment and/or maintenance of chromat.
GO; GO:0006325; P:negative regulation of transcriptional prei.
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 Length 180;
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 93.6%; Score 103; DB 1;
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RATARAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Radota K., Matsuda H.A., Sasi C., King B., Kochiwa H.,

Radota K., Matsudi P., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashiav-Sati V.
 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
library, clone:C430013M12 product:high mobility group box 1, full
name+Imob¹.
 STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 STRAIN=C57BJ/6J; TISSUB=Whole body; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nupmatization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CSTBL/60; TISSUE=Whole body;
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Shibata K., Itoh M., Alazawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 "Functional annotation of a full-length mouse cDNA collection.";
 181 AA
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 Nature 409:685-690(2001)
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 NUCLEOTIDE SEQUENCE
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 Name=Hmgbl;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Arizawa K., Hangashida K., Hayashida Y., Hiramoto K., Hiramoka T., Hirozane T., Aratoh H., Kawai J., Kondo K., Komno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okasuki Y., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shi
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rwish integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
 GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003235; F:nitric-oxide synthase regulator activity; IDA.
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HIACETO; IRRO00135; Highmoblty 12.
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NUCLEOTIDE SEQUENCE.
 P07156; 1NHN.
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 NCBI_TaxID=9606;
 NON TER
SEQUENCE
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Hypothetical protein. SEQUENCE 206 AA; 2
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 MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youchan J.W., Green B.D., Dickson M.C., Ablakealey R.W., Touchman J.W., Green B.D., Dickson M.C., Ablakealey R.W., Touchman J.W., Schmutz J., Myers R.M., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones W.A., Marra M.A., Schein J.B., Jones W.A., Schein J.B., Jones W.A., Schein J.B., Jones W.A., Schein J.B., Jones W.A., Marra M.A., Schein J.B., Jones W.A., Schein J.B., Jones W.A.
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310 00-97-3124
310 00-97-3124
31
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CURRENT FILING DATE: 1999-06-07
 US-09-949-016-10813
 SOFTWARE: Pat
SEQ ID NO 5
LENGTH: 214
 JS-09-214-881A-5
 US-09-214-881A-5
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 Gaps
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 APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usuari, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: ARANO, Kazuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Oshida, Junko)
FILE REFERENCE: 068843, Dudy
FILE REFERENCE: 068833.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
 APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Uesuqi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Okazaki, Takahiro
APPLICANT: Nakao, Kazuwa
APPLICANT: Sobida, Michiteru
APPLICANT: Sobida, Michiteru
APPLICANT: Sobida, Michiteru
APPLICANT: Osakada, Pumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REBERBENE: 068383.0104
CURRENT APPLICATION NUMBER: 1999-06-07
NUMBER OF SEQ ID NOS: 13
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TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
 Query Match 93.6%; Score 103; DB 2; Length 214; Best Local Similarity 95.0%; Pred. No. 5.2e-09; Matches 19; Conservative 0; Mismatches 1; Indels
 93.6%; Score 103; DB 2; Length 214; 95.0%; Pred. No. 5.2e-09; Live 0; Mismatches 1; Indels
 FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 214
 Sequence 4, Application US/09214881A
Patent No. 6822078
GENERAL INFORMATION:
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Yoshida, Michiteru
 FKDPNAPKRPPSAFFLFCSE 107
 Sequence 3, Application US/09214881A Patent No. 6822078
 88 FKDPNAPKRPPSAFFLFCSE 107
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Patentin Ver. 2.1
 Query Match
Best Local Similarity 95.0%
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-881A-1
 TYPE: PRT
ORGANISM: Bos taurus
 SOFTWARE: Pate
SEQ ID NO 3
 RESULT 3
US-09-214-881A-3
 US-09-214-881A-3
 RESULT 4
US-09-214-881A-4
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Sequence 10813, Application US/09949016

Fatent No. 6812339

GRNERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 10813
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 Gaps
 APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Okazaki, Hiroko
APPLICANT: Okazaki, Hiroko
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Rizuwa
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT PAPLICALION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
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 93.6%; Score 103; DB 2; Length 214; 95.0%; Pred. No. 5.2e-09; tive 0; Mismatches 1; Indels
 Query Match 93.6%; Score 103; DB 2; Length 214; Best Local Similarity 95.0%; Pred. No. 5.2e-09; Matches 19; Conservative 0; Mismatches 1; Indels
 Sequence 5, Application US/09214881A Patent No. 6822078
 88 PKDPNAPKRPPSAFFLFCSE 107
 88 FKDPNAPKRPPSAFFLFCSE 107
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
NUMBER OF SEQ 1D NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 214
TYPE: PRT
 Patentin Ver. 2.1
 Query Match
Best Local Similarity 95.0'
Matches 19; Conservative
 TYPE: PRT
ORGANISM: Rattus rattus
 ; ORGANISM: Sus scrofa
US-09-214-881A-4
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GENERAL INFORMATION:
 US-09-214-881A-2
 JS-09-214-881A-6
 US-09-214-881A-6
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 US-09-538-092-1018

Sequence 1018, Application US/09538092

Sequence 1018, Application US/09538092

Sequence 1018, Application US/09538092

Sebustal INPORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfeled, Traci A.
TITLE OF INVENTION: Procein-Protein Complexes and Method of Using Same TILE REFERENCE: 15966-542

CURRENT PAPLICATION NUMBER: US/09/538,092

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURPACTOR NUMBER: 60/178,965

SEQ ID NO 1018

LENGTH: 208
 Gaps
 ö
 APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Gaakada, Fumio
TILLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REPERENCE: G68383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
 Query Match 90.9%; Score 100; DB 2; Length 213; Best Local Similarity 94.7%; Pred. No. 1.6e-08; Matches 18; Conservative 0; Mismatches 1; Indels
 88.2%; Score 97; DB 2; Length 206; 94.7%; Pred. No. 4.8e-08; tive 0; Mismatches 1; Indels
 Sequence 9, Application US/09214881A Patent No. 6822078 GENERAL INFORMATION:
 91 FXDPNAPKRTPSAFFLFCS 109
 KDPNAPKRPPSAFFLFCSE 107
 1 FKDPNAPKRLPSAFFLFCS 19
 APPLICANT: Czaki, Shoichi
, APPLICANT: Sobajima, Junko
, APPLICANT: Useugi, Hiroko
, APPLICANT: Tanaka, Masao
, APPLICANT: Tanaka, Masao
, APPLICANT: Yoshida, Mi--
, APPLICANT: Yoshida, Mi--
, APPLICANT: Shi--
 2 KDPNAPKRLPSAFFLFCSE 20
 18; Conservative
 TYPE: PRT
ORGANISM: Gallus gallus
 TYPE: PRT
ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
LOCATION: (0)...(0)
 Best Local Similarity
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813
 SEQ ID NO 9
 US-09-214-881A-9
 US-09-214-881A-9
 Query Match
 FEATURE:
 Matches
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 APPLICANT: SCAAL, SHOLELL,
APPLICANT: Obacina, Junko
APPLICANT: Okazaki, Takahiro
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 06383.0104
CURRENT APPLICANTON NUMBER: US/09/214,881A
CURRENT PILING DATE: 1999-06-07
NUMBER, OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 208
 ö
 ö
 APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Sobajima, Junko
APPLICANT: Usavaji, Hiroko
APPLICANT: Oxazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Osahida, Michiteru
APPLICANT: Shirakawa, Hichshi
APPLICANT: Osakada, Fumio
TILE REFRENCE: 06383.0104
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOUTHARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 209
 Length 208;
 1; Indels
 1; Indels
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018
 Score 97; DB 2; 1
Pred. No. 4.8e-08;
0; Mismatches 1
 Score 97; DB 2;
Pred. No. 4.8e-08;
0; Mismatches 1
 Sequence 2, Application US/09214881A Patent No. 6822078
 Sequence 6, Application US/09214881A Patent No. 6822078
 89 KDPNAPKRPPSAFFLFCSE 107
 89 KDPNAPKRPPSAFFLFCSE 107
 2 KDPNAPKRLPSAFFLFCSE 20
 2 KDPNAPKRLPSAFFLFCSE 20
 Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
 Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
 GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
 ORGANISM: Homo sapiens
```

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Sequence 4826, Application US/09513999C

Sequence 4826, Application US/09513999C

Patent No. 6783961

GENERAL: INFORMATION:
APPLICANT: Dunds Mine Edwards, J.B.
APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

FILE REFREENCE: 59. US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 4826

LENGTH: 59
 88.2%; Score 97; DB 2; Length 879; 90.0%; Pred. No. 2.3e-07; Live 0; Mismatches 2; Indels
 Query Match 87.3%; Score 96; DB 2; Length 59; Best Local Similarity 90.0%; Pred. No. 1.8e-08; Matches 18; Conservative 0; Mismatches 2. Tarala
 Sequence 38, Application US/09914259
Fatent No. 6495336
GENERAL INFORMATION:
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE REFERENCE: 8471-010-999
CURRENT FILION NUMBER: US/09/914,259
CURRENT FILION DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 879
 RESULT 15
90.09-513-99C-4824
Sequence 4824, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: DUMMS Milne Edwards, J.B.
PAPLICANT: DUMMS Milne Edwards, J.B.
PAPLICANT: DUMDE DUMPS MILDE
 763 FKDPNAPKRPPLAFFLFCSE 782
 201 KDPNAPKRPPSAFFLFCSE 219
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 38 FKGPNAPKRPPSAFFLFCSE 57
 20
 2 KDPNAPKRLPSAFFLFCSE
 Query Match
Best Local Similarity 90.05
Matches 18; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-914-259-38
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 14:
US-09-513-999C-4826
 US-09-513-999C-4826
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 RESULT 12
US-09-949-016-10728

J Sequence 10728, Application US/09949016

REGURNATION: 0612339

GENERAL INFORMATION: TO Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FEASTSEQ FOR Windows Version 4.0

SEQ ID NO 10728
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 APPLICANT: Shirkawa, Hitoshi
APPLICANT: Shirkawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 209
/ Match 88.2%; Score 97; DB 2; Length 209; Local Similarity 94.7%; Pred. No. 4.8e-08; Nes 18; Conservative 0; Mismatches 1; Indels
 Query Match 88.2%; Score 97; DB 2; Length 209; Best Local Similarity 94.7%; Pred. No. 4.8e-08; Matches 18; Conservative 0; Mismatches 1; Indels
 Length 320;
 88.2%; Score 97; DB 2; Length 320
94.7%; Pred. No. 7.7e-08;
iive 0; Mismatches 1; Indels
 Sequence 8, Application US/09214881A
Patent No. 6822078
GENERAL INPORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
 89 KDPNAPKRPPSAFFLFCSE 107
 89 KDPNAPKRPPSAFFLFCSE 107
 2 KDPNAPKRLPSAFFLFCSE 20
 2 KDPNAPKRLPSAFFLFCSE 20
 APPLICANT: Ozaki, Shoichi
APPLICANT: Ozaki, Shoichi
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaha, Masao
APPLICANT: Tanaha, Masao
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa uiteru
APPLICANT: Shirakawa uiteru
 Query Match
Best Local Similarity 94.7
Matches 18; Conservative
 TYPE: PRT ORGANISM: Rattus rattus
 ; ORGANISM: Human
US-09-949-016-10728
 US-09-214-881A-8
 US-09-214-881A-8
 Query Match
 TYPE: PRT
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Matches
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Gaps

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 Query Match 87.3%; Score 96; DB 2; Length 110; Best Local Similarity 90.0%; Pred. No. 3.5e-08; Matches 18; Conservative 0; Mismatches 2; Indels
 89 FKXPNAPKRPPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
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Search completed: April 6, 2006, 10:27:51 Job time : 6.72368 secs

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Sequence 23, Application US/10300072
Publication No. US20030144201A1
GENERAL INFORMATION:
APPLICANT: Hoan Yang
APPLICANT: Hoan Yang
APPLICANT: Hoal Abaw Warren, Jr.
APPLICANT: Hoal Shaw Warren, Jr.
APPLICANT: Mitchell P. Fink
TITLE OF INVENTION: AGENTS
FILE REPERENCE: 3269.1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 10/147,447
PRIOR PILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,034
 tch 100.0%; Score 110; DB 4; Length 20; al Similarity 100.0%; Pred. No. 2.4e-09; 20; Conservative 0; Mismatches 0; Indels
 US-10-147-447-16

US-10-147-447-16

Sequence 16, Application US/1014747

Publication No. US20030060410A1

GENERAL INFORMATION:
APPLICANT: Tracey, Kevin J.
APPLICANT: Yang, Huan
APPLICANT: Warren Jr., Howland Shaw
TITLE OF INVENTION: Use of HMG Fragments as
TITLE OF INVENTION: Anti-Inflammatory Agents
TITLE OF INVENTION: Anti-Inflammatory Agents
TITLE OF INVENTION: Anti-Inflammatory Agents
TURRENT APPLICATION NUMBER: US/10/147,447

CURRENT APPLICATION NUMBER: 60/291,034

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR PRILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20
 US-10-456-947-10
US-10-718-495-18
US-10-717-984-18
US-10-717-984-24
US-10-717-984-24
US-10-300-072-54
US-10-300-072-54
US-10-456-947-42
US-10-456-947-42
US-10-456-947-42
US-10-718-495-54
US-10-718-495-54
US-10-718-495-54
 US-10-717-984-54
 ALIGNMENTS
 1 FKDPNAPKRLPSAFFLFCSE 20
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 20; Conserv
1000.0
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 US-10-147-447-16
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 (without alignments)
439.516 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 16,
 April 6, 2006, 10:26:34 ; Search time 19.0132 Seconds
 Description
 Sequence
Sequence
Sequence
Sequence
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Sequence
Sequence
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 Published Applications_AA_Main:*
(Ggn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*): /Ggn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(Ggn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*): /Ggn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*
(Ggn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*): /Ggn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*): /Ggn2_6/ptodata/1/pubpaa/USII_PUBCOMB.pep:*
 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
 US-10-300-072-23
US-10-456-949-16
US-10-718-495-23
US-10-717-984-23
US-10-717-984-23
US-10-300-072-53
US-10-456-947-8
US-10-456-947-8
US-10-456-947-8
US-10-718-495-23
US-10-718-495-23
US-10-718-495-53
US-10-718-495-53
US-10-718-495-53
US-10-718-495-53
US-10-718-495-53
US-10-718-495-53
US-10-718-798-53
US-10-718-798-53
US-10-718-798-53
US-10-718-798-79
US-10-718-798-79
US-10-718-798-19
US-10-718-798-19
 Total number of hits satisfying chosen parameters:
 1867569 segs, 417829326 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 110
1 FKDPNAPKRLPSAFFLFCSE 20
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-10-717-984-23
 Query
Match Length
 100.0
 100.0
 100.0
 100.0
 Scoring table:
 Perfect score:
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Gaps

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Gaps

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Indels

Length 20;

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; Score 110; DB 4;
; Pred. No. 2.4e-09;
0; Mismatches 0;
 RESULT 5
US-10-718-495-23
Sequence 23, Application US/10718495
Publication No. US20040141948A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa L.
TITLE OF INVENTION: USE OF HAGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: US/10/718,495
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR RILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 23
LENGTH: 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
 ; ORGANISM: Homo Sapiens
US-10-456-947-45
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 6
US-10-717-984-23
 RESULT 7
US-10-147-447-20
 US-10-718-495-23
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 RESULT 4

US-10-456-947-45

i Sequence 45, Application US/10456947

i Sequence 45, Application US/10456947

j Publication No. US20040053841A1

j GENERAL INFORMATION:

i APPLICANT: Kevin J. Tracey

i TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

i TITLE OF INVENTION: HAGB POLYBEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

i TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

i FILE REFERENCE: 3268.1001-007

i CURRENT APPLICATION NUMBER: US/10/456,947

CURRENT FILING DATE: 2002-05-15

i RIOR APPLICATION NUMBER: 60/291,034

pRIOR FILING DATE: 2001-05-15

i NUMBER OF SEQ ID NOS: 46

i SEQ ID NOS: 46

i EMOTH: 20

i TYPE: PRT
 Gaps
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 Query Match

100.0%; Score 110; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e-09;

Matches 20; Conservative 0; Mismatches 0; Indels
 ch 100.0%; Score 110; DB 4; Length 20; Similarity 100.0%; Pred. No. 2.4e-09; 20; Conservative 0; Mismatches 0; Indels
 US-10-456-949-16
Squence 16, Application US/10456949
Publication No. US20040005316A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3269.1001-006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: 10/147,447
PRIOR APPLICATION NUMBER: 60/291,034
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-23
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 20; Conserv
 US-10-456-949-16
 SEQ ID NO 16
LENGTH: 20
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Query Match 100.0%; Score 110; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 2.4e-09; Matches 20; Conservative 0; Mismatches 0; Indels
 Length 20;
 Indels
 TITLE OF INVENTION: Walter

TITLE OF INVENTION: HAGEL COMBINATION THERAPIES

FILE REFERENCE: 3.258.1008-001

CURRENT APPLICATION NUMBER: US/10/717,984

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 00/277,846

PRIOR APPLICATION NUMBER: 00/277,846

PRIOR APPLICATION NUMBER: 01/20

INVERSE OF TILING DATE: 2002-11-20

SEQ ID NOS: 58

LENGTH: 20

ILENGTH: 20

TYPE: PRI CORGANISM: Home sapiens

US-10-717-984-23
 Query Match
100.0%; Score 110; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0;
 ; Sequence 23, Application US/10717984; Publication No. US20040156851A1; GENERAL INFORMATION:
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
```

```
Sequence 8, Application US/10456947
Publication No. US20040053841A1
GENERAL INFORMATION:
APPLICANT: Huan Yang
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3266.1001-007
CURRENT APPLICATION NUMBER: US/10/456,947
 ö
 ö
 APPLICANT: Matchell P. Fink
TITLE OF INVENTION: USE OF HWGB FRAGMENTS AS ANTI-FLAMMATORY
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 3268-1001-005
CURRENT APPLICATION NUMBER: US/10/300,072
CURRENT PILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 00/291,034
PRIOR APPLICATION NUMBER: US 00/291,034
PRIOR APPLICATION NUMBER: US 00/291,034
PRIOR PELLING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 74
 Query Match
100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 110; DB 4; Length 74; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 20; Conservative 0; Mismatches 0; Indels
 Sequence 20, Application US/10456949
Fublication No. US20040005316A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Huan Yang
ITILE OF INVENTION: USE OF HMG FRACHENTS AS
ITILE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3268.1001.006
CURRENT APPLICATION NUMBER: US/10/456,949
CURRENT APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
FRIOR FILING DATE: 2001-05-15
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
 Howland Shaw Warren, Jr.
 1 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 FKDPNAPKRLPSAFFLFCSE 20
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo Sapien
US-10-456-949-20
 JS-10-456-949-20
 US-10-300-072-53
 RESULT 11
US-10-456-947-8
 SEQ ID NO 20
LENGTH: 74
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 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Huan Yang

APPLICANT: Howland Shaw Warren, Jr.

TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAWMATORY

TITLE OF INVENTION: AGENTS

TITLE OF INVENTION: AGENTS

CURRENT APPLICATION NUMBER: US/10/300,072

CURRENT FILING DATE: 2002-11-20

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2001-05-15

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 74
 100.0%; Score 110; DB 4; Length 74; 100.0%; Pred. No. 9.6e-09; tive 0; Mismatches 0; Indels
 Length 74;
 0; Indels
 100.0%; Score 110; DB 4;
100.0%; Pred. No. 9.6e-09;
tive 0; Mismatches 0;
 APPLICANT: Yang, Huan
APPLICANT: Yang, Huan
APPLICANT: Yang, Huan
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Warren Jr., Howland Shaw
APPLICANT: Pink, Mitchell P.
TITLE OF INVENTION: Matchell P.
TITLE OF INVENTION: Anti-Inflammatory Agents
TITLE OF INVENTION: Anti-Inflammatory Agents
TITLE OF INVENTION: Anti-Inflammatory Agents
TITLE OF INVENTION: NUMBER: US/10/147,447
CURRENT FILING DATE: 2002-08-16
PRIOR PILLING DATE: 2002-08-16
PRIOR FILING DATE: 201-05-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
 ; Sequence 53, Application US/10300072; Publication No. US20030144201A1; GENERAL INFORMATION: APPLICANT: Kevin J. Tracey; APPLICANT: Huan Yang
Sequence 20, Application US/10147447
Publication No. US20030060410A1
GENERAL INFORMATION:
 RESULT 8
US-10-300-072-20
Sequence 20, Application US/10300072
Publication No. US20030144201A1
GENERAL INFORMATION:
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 PKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Query Match
Best Local Similarity 100.
Matches 20; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-147-447-20
 TYPE: PRT
ORGANISM: Homo sapiens
 US-10-300-072-53
 US-10-300-072-20
 SEQ ID NO 20
LENGTH: 74
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Gaps

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Search completed: April 6, 2006, 10:32:46
 ; ORGANISM: Homo sapiens
US-10-718-495-20
 US-10-718-495-53
 US-10-718-495-53
 US-10-717-984-20
; TYPE: PRT
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 Sequence 39, Application US/10456947

Sequence 39, Application US/10456947

Publication No. US20040053841A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Tracey

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN

TITLE OF INVENTION: Had POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: HAGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: HAMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS

TITLE OF INVENTION: HAMBER: US/10/456,947

CURRENT APPLICATION NUMBER: US/10/47,447

PRIOR PILING DATE: 2002-05-15

PRIOR APPLICATION NUMBER: 60/291,034

PRIOR PILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 74
 Gaps
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 Length 74;
 Query Match 100.0%; Score 110; DB 4; Length 74; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 20; Conservative 0; Mismatches 0; Indels
 0; Indels
 100.0%; Score 110; DB 4;
100.0%; Pred. No. 9.6e-09;
Live 0; Mismatches 0;
 Sequence 20, Application US/10718495

Publication No. US20040141948A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: ARTI-INFLAMMATORY AGENTS

TITLE OF INVENTION: ARTI-INFLAMMATORY AGENTS

CURRENT APPLICATION NUMBER: US/10/718,495

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: 60/427,841

PRIOR APPLICATION NUMBER: 60/427,841

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PASKEQ for Windows Version 4.0

SEQ ID NO 20
 PRIOR APPLICATION NUMBER: 10/147,447
PRIOR FILING DATE: 2002-05-15
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 8
LENGTH: 74
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 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
CURRENT FILING DATE: 2003-06-06
 Query Match
Best Local Similarity 100.0
Matches 20; Conservative
 TYPE: PRT
ORGANISM: Homo Sapiens
 t TYPE: PRT
CORGANISM: Homo Sapiens
US-10-456-947-39
 RESULT 12
US-10-456-947-39
 RESULT 13
US-10-718-495-20
 US-10-456-947-8
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 Gaps
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Query Match
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
 100.0%; Score 110; DB 4; Length 74; 100.0%; Pred. No. 9.6e-09; ive 0; Mismatches 0; Indels
 Length 74;
 Indels
 Sequence 20, Application US/10717984

Publication No. US20040156851A1

GENERAL INFORMATION

APPLICATOR Newman, Waler

TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES

FILE REFERENCE: 3281.000-001

CURRENT APPLICATION NUMBER: US/10/717,984

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR APPLICATION NUMBER: 60/427,846

PRIOR PRIUNG DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 20

SEQ ID NO 20

LENGTH: 74
 Query Match
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0;
 Sequence 53, Application US/10718495
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
FILE REFERENCE: 3258.1009-001
CURRENT APPLICATION NUMBER: 0S/10/718,495
PRIOR APPLICATION NUMBER: 60/427,841
PRIOR FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-2

NUMBER OF SEQ ID NOS: 58
SOFTWARE: RastSEQ for Windows Version 4.0

LENGTH: 74
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Query Match
Best Local Similarity 100.0
Matches 20; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
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Job time : 20.0132 secs

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1443
US-10-821-234-1443
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 1234, Ap
1192, App
1192, App
3073, Ap
1105, Ap
1105, Ap
313, App
1156, Ap
1156, Ap
1151, Ap
 April 6, 2006, 10:28:08; Search time 2.5 Seconds (without alignments) 249.536 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 Sequence 1
Sequence 1
Sequence 1
Sequence 2
Sequence 3
 Sequence Seq
 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
 Published Applications AA New:*

1. /SIDS5/ptodata/2/pubpaa/US08_NEW PUB.pep:*
2. /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
3. /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4. /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5. /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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7. /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8. /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
 US-11-096-568A-9681
US-11-172-740-1564
US-11-096-568A-9680
US-11-096-568A-15615
 US-10-821-234-1443

US-11-186-422-13

US-11-186-422-13

US-11-169-041-192

US-11-169-041-192

US-11-087-099-3073

US-11-087-099-105

US-11-087-099-105

US-11-087-099-1105

US-11-087-099-1105

US-11-172-740-1565

US-11-172-740-1565

US-11-172-740-1569

 Total number of hits satisfying chosen parameters:
 184161 segs, 31191982 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 110
1 FKDPNAPKRLPSAFFLFCSE 20
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-10-717-984-23
 Query
Match Length DB
 Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 Run on:
 Result
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 JUNE AND TOTAL STATE AND TOTAL
Sequence 15614, A Sequence 9518, App Sequence 9518, App Sequence 1572, App Sequence 1572, App Sequence 1572, App Sequence 10060, A Sequence 10515, A Sequence 10515, A Sequence 10535, A Sequence 10535, A Sequence 11987, A Sequence 11126, A Sequence 11987, A Sequence 11126, A Sequence 1126, A Sequence 11126, A Sequence 1126, A Sequence 1126, A Sequence 1
 Sequence 4210,
Sequence 2173,
 Gaps
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 Length 215;
 Indels
 US-11-097-099-869
US-11-097-099-869
US-11-172-740-1563
US-11-172-740-1563
US-11-087-099-2564
US-11-087-099-8838
US-11-087-099-6594
US-11-087-099-6594
US-11-096-568A-13611
US-11-096-568A-13611
US-11-096-568A-1688
US-11-096-568A-1688
US-11-087-099-11987
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US-11-087-099-11087
US-11-087-099-11087
 93.6%; Score 103; DB 6; L 95.0%; Pred. No. 3.2e-09; tive 0; Mismatches 1;
 US-11-186422-11
Sequence 11, Application US/11186422
Sequence 11, Application US/11186422
FUBLICATION NO. US20060057679A1
GENERAL INFORMATION:
APPLICANT: Critical Therapeutics, Inc.
APPLICANT: Oreefe, Theresa
APPLICANT: Oreefe, Theresa
APPLICANT: Oreefe, Theresa
TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
FILE REFERENCE: 3258-1021-003
CURRENT APPLICATION NUMBER: US/11/186,422
CURRENT PILING DATE: 2005-07-20
FRIOR APPLICATION NUMBER: 60/589,678
PRIOR PILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 34
 ALIGNMENTS
 1 FKDPNAPKRLPSAFFLFCSE 20
 93.0
Best Local Similarity 95.0
Matches 19; Conservative
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```
DEFICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
FILE REFERENCE: 10001 NP
FILE REFERENCE: 2004-05
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR APPLICATION NUMBER: 60/584,405
NUMBER OF SEQ ID NOS: 527
SOFTWARE: Patentin version 3.2
SEQ ID NO 192
LENGTH: 879
 Gaps
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 Length 169;
 Length 879;
 Length 69;
 Query Match 88.2%; Score 97; DB 7; Length 875
Best Local Similarity 90.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 2; Indels
 Score 79; DB 7; Length 69;
Pred. No. 7.1e-06;
0; Mismatches 1; Indels
 Score 97; DB 6; I
Pred. No. 2.3e-08;
0; Mismatches 1;
 Sequence 14, Application US/11186422

Publication No. US20060057679A1

GENERAL INFORMATION:

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: Critical Therapeutics, Inc.

APPLICANT: Unciano, Peter

APPLICANT: Qin Shixin

TILE OF INVENTION: RAGE PROTEIN DERIVATIVES

FILE PERERENCE: 3258.1021-003

CURRENT APPLICATION NUMBER: US/11/186,422

CURRENT APPLICATION NUMBER: 05/599,678

PRIOR APPLICATION NUMBER: 60/589,678

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
 US-11-169-041-192
. Sequence 182, Application US/11169041
. Publication No. US20060019284A1
. GENERAL INFORMATION:
 763 FKDPNAPKRPPLAFFLFCSE 782
 1 FKDPNAPKRLPSAFFLFCSE 20
 77 KDPNAPKRPPSAFFLFCSE 95
 2 KDPNAPKRLPSAFFLFCSE 20
 Query Match 88.2%;
Best Local Similarity 94.7%;
Matches 18; Conservative
 5 NAPKRLPSAFFLFCSE 20
 1 NAPKRPPSAFFLFCSE 16
 Query Match
71.8%;
Best Local Similarity 93.8%;
Matches 15; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-11-169-041-192
 ORGANISM: Homo sapiens
 US-10-821-234-1234
 JS-11-186-422-14
 US-11-186-422-14
 RESULT 5
 RESULT 6
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 Sequence 1234, Application US/10821234

| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat. Ivan
| APPLICANT: Andarmai, Susan
| APPLICANT: Andarmai, Susan
| APPLICANT: Tang, Y. Tom
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| FILE REFERENCE: 821A
| CURRENT APPLICATION NUMBER: US/10/821,234
| CURRENT FILING DATE: 2004-04-07
| PRIOR PILING DATE: 2003-04-07
| PRIOR FILING DATE: 2003-04-07
| NUMBER OF SEQ ID NOS: 1704
| SOFTWARE: PL SEQ_Genes Version 1.0
| SEQ ID NO 1234
| TENOTH: 169
| TYPE: PRIOR PERFORMATION NUMBER: US NOT NO 1234
| TENOTH: 169
| TYPE: PRIOR PERFORMATION NUMBER: US NOT NO 1234
| TENOTH: 169
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 93.6%; Score 103; DB 7; Length 215; 95.0%; Pred. No. 3.2e-09; Live 0; Mismatches 1; Indels
 Query Match

93.6%; Score 103; DB 7; Length 215;
Best Local Similarity 95.0%; Pred. No. 3.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels
 NAME/KEY: misc feature
LOCATION: (1)...(169)
OTHER INFORMATION: Xaa = any amino acid or nothing
 APPLICANT: O'Reefe, Theresa APPLICANT: Luciano, Peter APPLICANT: Luciano, Peter APPLICANT: Luciano, Peter TITLE OF INVENTION: SAIATIN
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11
 Sequence 12, Application US/11186422
Publication No. US20060057679A1
GENERAL INCRMATION:
APPLICANT: Critical Therapeutics, Inc.
 FKDPNAPKRPPSAFFLFCSE 108
 89 FKDPNAPKRPPSAFFLFCSE 108
 1 FKDPNAPKRLPSAFFLFCSE 20
 1 FKDPNAPKRLPSAFFLFCSE 20
 Conservative
 SEQ ID NO 12
LENGTH: 215
TYPE: PRT
ORGANISM: Mus musculus
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 Best Local Similarity
Matches 19; Conserv
 RESULT 4
US-10-821-234-1234
 RESULT 3
US-11-186-422-12
 US-11-186-422-11
 US-11-186-422-12
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 US-11-087-099-4976
US-11-087-099-4976
Sequence 4976, Application US/11087099
Sequence 4976, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4976
LEASTH: 142
 US-11-07-099-313

US-11-07-099-313

Sequence 313, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

TITLE OF INVENTION: Gene and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450) B P

CURRENT ADDLICATION UNMERR: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 313
 Score 75; DB 7; Length 141;
Pred. No. 6.3e-05;
1; Mismatches 4; Indels
 Score 75; DB 7; Length 142; Pred. No. 6.3e-05; 1; Mismatches 4; Indels
 Indels
 4
1; Mismatches
 41 KDPNKPKRPPSAFFVFMEE 59
 2 KDPNAPKRLPSAFFLFCSE 20
 31 KDPNKPKRPPSAFFVFMEE 49
 31 KDPNKPKRPPSAFFVFMEE 49
 2 KDPNAPKRLPSAFFLFCSE 20
 2 KDPNAPKRLPSAFFLFCSE 20
 Query Match 68.2%;
Best Local Similarity 73.7%;
Matches 14; Conservative
 Query Match 68.2%;
Best Local Similarity 73.7%;
Matches 14; Conservative
 ; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-9185
 ; ORGANISM: Nicotiana tabacum
US-11-087-099-4976
14; Conservative
Matches
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 RESULT 8
US-11-087-099-1105
; Sequence 1105, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTYON: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21 (53450) B EP; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1105
. LENGTH: 160
 Score 77; DB 7; Length 160;
Pred. No. 3.4e-05;
1; Mismatches 4; Indels
 Score 75; DB 7; Length 106; Pred. No. 4.7e-05;
 Length 141;
 Sequence 3073, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPREBRUCE: 38 – 21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3073
LENGTH: 141
 Sequence 7075, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 106
 71.8%; Score 79; DB 7; I
78.9%; Pred. No. 1.4e-05;
Live 1; Mismatches 3;
 ; TYPE: PRT
; ORGANISM: Narcissus pseudonarcissus
US-11-087-099-7075
 2 KDPNAPKRLPSAFFLFCSE 20
 32 KDPNKPKRPPSAFFVFMSE 50
 KDPNKPKRAPSAFFVFMGE 55
 2 KDPNAPKRLPSAFFLFCSE 20
 68.28;
 Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative
 ; ORGANISM: Canavalia gladiata
US-11-087-099-3073
 Conservative
 Best Local Similarity
Matches 15; Conserv
 Query Match
Best Local Similarity
 US-11-087-099-7075
 US-11-087-099-3073
 TYPE: PRT ORGANISM:
 Query Match
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Sequence 1566, Application US/11172740 Publication No. US20060057724A1
 FEATURE:
NAME/KEY: misc_feature
 NAME/KEY: misc_feature LOCATION:
 NAME/KEY: misc_feature LOCATION:
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
 US-11-087-099-3510
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 RESULT 13
US-11-172-740-1565

1 Sequence 1565, Application US/11172740

2 Publication No. US20060057724A1

3 GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: DVINGERIN UNCLEOTIDE SEQUENCES AND PHENOTYPES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES

CURRENT APPLICATION NUMBER: 05/583,621

PRIOR FILING DATE: 2004-06-30

PRIOR PELING DATE: 2004-06-30

PRIOR PELING DATE: 2004-06-30

PRIOR PELING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

NUMBER OF SEQ ID NOS: 2523

SEQ ID NO 1565

LENGTH: 152
 OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
 OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowed
 OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
 OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
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 . LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1565
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 Score 75; DB 7; Length 152; Pred. No. 6.7e-05; 1; Mismatches 4; Indels
 Query Match 68.2%; Score 75; DB 7; Length 152; Best Local Similarity 73.7%; Pred. No. 6.7e-05; Matches 14; Conservative 1; Mismatches 4; Indels
 NAME/KEY: misc feature
LOCATION: (1). [152)
OTHER INFORMATION: Ceres CLONE ID no. 721511
 2 KDPNAPKRLPSAFFLFCSE 20
 39 KDPNKPKRPPSAFFVFMEE 57
 2 KDPNAPKRLPSAFFLFCSE 20
 39 KDPNKPKRPPSAFFVFMEE 57
 Query Match
Best Local Similarity 73.7%;
Matches 14; Conservative
 NAME/KEY: misc_feature
 WAME/KEY: misc_feature
 FEATURE:
NAME/KEY: misc_feature
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
; ORGANISM: Glycine max US-11-087-099-313
 ORGANISM: Glycine max
 LOCATION:
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RESULT 14 US-11-172-740-1566

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GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: BROWER, Vyacheelav
ITILE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE REFERENCE: 2750-1602PUS2
CURRENT APPLICATION NUMBER: US/11/172,740
PRIOR FILING DATE: 2004-06-30
PRIOR PELLING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 1566
LENGTH: 152
 OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying fruit
 OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confinen
 OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowers
 OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
 ; OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1566
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 Query Match 68.2%; Score 75; DB 7; Length 152; Best Local Similarity 73.7%; Pred. No. 6.7e-05; Matches 14; Conservative 1; Mismatches 4; Indels
 Sequence 3510, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
ITILE OF INVENTION: Genes and Uses for Plant Improvement
FIRE REPREBENCE: 32-21(55450) B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 3510
LENGTH: 149
 LOCATION: (1). (152)
OTHER INFORMATION: Public GI no. 18645
 2 KDPNAPKRLPSAFFLFCSE 20
 39 KDPNKPKRPPSAFFVFMEE 57
 ; TYPE: PRT;
; ORGANISM: Vicia faba
US-11-087-099-3510
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 0; Gaps
Query Match

66.4%; Score 73; DB 7; Length 149;
Best Local Similarity 68.4%; Pred. No. 0.00014;
Matches 13; Conservative 3; Mismatches 3; Indels
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Search completed: April 6, 2006, 10:33:30 Job time: 3.5 secs

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